

GenCore version 5.1.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 20, 2006, 20:29:34 ; Search time 1060 Seconds

(without alignments)
4288.038 Million cell updates/sec

Title: US-10-782-096-2

Perfect score: 3597

Sequence: 1 MNSYKNKNEYMLDALRINS.....TFPNOSLEKREQEVDNLFIN 682

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cpn2.1/USPTO.spool/US10782096/runat.20012006.095214.24386/app_query.fasta_1.839
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosom62 -TRANS=human40.coi -LIST=45
-DOCALIGN=200 -NORM=ext -HEAPSIZ=500 -MINLEN=0 -ALIGN=15 -MODE=LOCAL
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-NO WMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -DEV TIMEOUT=120 -WARN TIMEOUT=30
-THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq 21.1*

1: Geneseqn1980bs:*
2: Geneseqn1990bs:*
3: Geneseqn2000bs:*
4: Geneseqn2001as:*
5: Geneseqn2002as:*
6: Geneseqn2002bs:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2003ds:*
11: Geneseqn2004as:*
12: Geneseqn2004bs:*
13: Geneseqn2005as:*
14: Geneseqn2005bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3597	100.0	2049	13 ADR89407	Adr89407 AXMI-009
2	3536	98.3	2016	13 ADR89409	Adr89409 AXMI-009
3	3488	97.0	1986	13 ADR89411	Adr89411 AXMI-009
4	948	26.4	3621	6 ABK87234	Abk87234 Bacillus

5	948	26.4	3621	12 ADL15304	Adl15304 B thuring
6	948	26.4	3621	14 AEB45606	Aeb45606 B. thurin
7	948	26.4	3621	14 AEB34684	Aeb34684 Bacillus
8	948	26.4	4874	6 ABK87247	Abk87247 Bacillus
9	948	26.4	4874	12 ADL15320	Adl15320 B thuring
10	948	26.4	4874	14 AEB45622	Aeb45622 B. thurin
11	942.5	26.2	3507	2 AAT43221	Aat43221 Antiscara
12	940.5	26.1	3690	6 ABK51132	Abk51132 cDNA enco
13	926	25.7	2003	6 ABK87236	Abk87236 Bacillus
14	926	25.7	2010	6 ABK87241	Abk87241 Bacillus
15	926	25.7	2010	6 ABK87238	Abk87238 Maize Opt
16	926	25.7	2010	12 ADL15308	Adl15308 B thuring
17	926	25.7	2010	12 ADL15314	Adl15314 B thuring
18	926	25.7	2010	14 AEB45610	Aeb45610 Maize-opt
19	926	25.7	2010	14 AEB45616	Aeb45616 B. thurin
20	925.5	25.7	2022	12 ADL15384	Adl15384 B thuring
21	925.5	25.7	2022	12 ADL15352	Adl15352 B thuring
22	925.5	25.7	2022	14 AEB45654	Aeb45654 B. thurin
23	925.5	25.7	2022	14 AEB45686	Aeb45686 B. thurin
24	925	25.7	2022	6 ABK87239	Abk87239 Bacillus
25	925	25.7	2022	12 ADL15336	Adl15336 B thuring
26	925	25.7	2022	12 ADL15310	Adl15310 B thuring
27	925	25.7	2022	12 ADL15328	Adl15328 B thuring
28	925	25.7	2022	12 ADL15332	Adl15332 B thuring
29	925	25.7	2022	12 ADL15372	Adl15372 B thuring
30	925	25.7	2022	14 AEB45638	Aeb45638 B. thurin
31	925	25.7	2022	14 AEB45612	Aeb45612 B. thurin
32	925	25.7	2022	14 AEB45634	Aeb45634 B. thurin
33	925	25.7	2022	14 AEB45630	Aeb45630 B. thurin
34	925	25.7	2022	14 AEB45674	Aeb45674 B. thurin
35	924.5	25.7	2022	12 ADL15378	Adl15378 B thuring
36	924.5	25.7	2022	12 ADL15346	Adl15346 B thuring
37	924.5	25.7	2022	14 AEB45648	Aeb45648 B. thurin
38	924.5	25.7	2022	14 AEB45680	Aeb45680 B. thurin
39	924	25.7	2025	12 ADL15348	Adl15348 B thuring
40	924	25.7	2025	12 ADL15380	Adl15380 B thuring
41	924	25.7	2025	14 AEB45682	Aeb45682 B. thurin
42	924	25.7	2025	14 AEB45650	Aeb45650 B. thurin
43	924	25.7	3633	6 ABK87235	Abk87235 Bacillus
44	924	25.7	3633	12 ADL15306	Adl15306 B thuring
45	924	25.7	3633	14 AEB45608	Aeb45608 B. thurin

ALIGNMENTS

RESULT 1	ADR89407	standard; cDNA; 2049 BP.
ID	ADR89407	standard; cDNA; 2049 BP.
XX	ADR89407;	
AC	ADR89407;	
DT	18-NOV-2004	(first entry)
XX	ADR89407;	
DE	AXMI-009	coding sequence.
XX	ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;	
KW	expression cassette; transformation; transgenic; plant; bacteria;	
KW	lepidoptera; coleoptera; pest; pesticide; resistance;	
KW	pesticidal activity.	
XX	Bacillus thuringiensis.	
OS	Bacillus thuringiensis.	
XX	Key	Location/Qualifiers
FH	CDS	1..2049
FT		/*tag= a
FT		/product= "AXMI-009"
XX	WO2004074462-A2.	
PD	02-SEP-2004.	
XX	20-FEB-2004; 2004WO-US005829.	
PF		
XX		

PR 20-FEB-2003; 2003US-0448632P.
 PR 20-FEB-2003; 2003US-0448633P.
 PR 20-FEB-2003; 2003US-0448797P.
 PR 20-FEB-2003; 2003US-0448806P.
 PR 20-FEB-2003; 2003US-0448810P.
 PR 20-FEB-2003; 2003US-0448812P.
 PR 19-FEB-2004; 2004US-00781979.
 PR 19-FEB-2004; 2004US-00782020.
 PR 19-FEB-2004; 2004US-00782096.
 PR 19-FEB-2004; 2004US-00782141.
 PR 19-FEB-2004; 2004US-00782570.
 PR 19-FEB-2004; 2004US-00783417.

XX (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargiss T, Kozziel MG, Duck NB, Carr B;

XX WPI; 2004-635574/61.

DR P-PSDB; ADR89408.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.

PS Claim 1; SEQ ID NO 19; 178pp; English.

XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.

XX SQ Sequence 2049 BP; 688 A; 316 C; 403 G; 642 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 2049
 Score: 3597.00 Matches: 682
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 13 Gaps: 0

US-10-782-096-2 (1-682) x ADR89407 (1-2049)

QY 1 MetAsnSerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSer 20
 DB 1 ATGAATTCATATAAAATATAAAATGAATATGAATGTTGGATGCTTTACGAATCAACTCT 60
 QY 21 AsnMetSerAsnCyTyTProArgTyrProLeuAlaLysAspProGlnMetThrMetArg 40
 DB 61 AATATGTCTAATTTGTTATCCAAAGGTATCCACTAGCAGAAAGATCCACAAATGACTATGGGA 120
 QY 41 AsnThrAsnTyrLysGluTyrLeuAsnMetCysAspSerAsnThrClnPheIleGlyAsp 60
 DB 121 AACACGAACCTATAAAGATGGCTAAATATGTGTGATTCAAATACACAAATTTATTTGGTGAT 180
 QY 61 IleSerThrTyrSerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGly 80
 DB 191 ATAAGCAGTATCTTAGCCCTGAAGCTGCTTTAAGTGTACGAGATGCTGTTTAAACGGGT 240
 QY 81 IleAsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPhe 100
 DB 241 ATTAACAGTGTAGGAGCTATACTTTTCCGAATTTAGGGGTCCTTTTGGCAAGTCAATCAATTT 300

QY 101 GlyIleIleSerArgLeuIleGlyIleLeuTyrAlaGlyProAspProPheGluAlaLeu 120
 DB 301 GGAATTAATTAGTAGCTAATAGGTATTTTATGGCAGGGCTGATCCATTTGAGCACTT 360
 QY 121 MetValLeuValGluGluLeuIleLysSerIleAspGlnArgValArgGluAsnAla 140
 DB 361 ATGGTTCCTGTTGAAGAGCTTATTAAAGAAAGTATAGATCAGCGTGTAAAGAGAAATGCT 420
 QY 141 LeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgGluAla 160
 DB 421 CTTAGAGAGCTAGAAAGGTTTACAGGGAATTATAGAGCTATATCAAACTAGACTGCAAGCA 480
 QY 161 TrpLeuValAsnLysAsnAspAsnArgAlaLeuValThrGlnTyrAlaIleVal 180
 DB 481 TGGCTAGTTAACAGAAATGATGACATCGAGGGCACTAGTAAACGAGTATGCAATGCTT 540
 QY 181 AspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeu 200
 DB 541 GATAAATTTTTTCGAAAGAAATATGCCAAAATTCAGGAAAGAAACTTTTGAATAATTTATTG 600
 QY 201 LeuProValTyrAlaGlnAlaAlaAsnLeuHisIleLeuLeuLeuArgAspAspTyr 220
 DB 601 TTACCGATATATGACAAAGCCCGCAATTTGCATTTAATTTTATTAAAGAGATGCTGATTAT 660
 QY 221 PheGlyAlaGlnTrpGlnLeuGlyAspGluIleArgAspAsnTyrIleArgLeuGln 240
 DB 661 TTTGGAGCAGCTGGCAATTAGGTGATGATGAATTCGTGATTAATTATATCAGACTACAA 720
 QY 241 GlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeuAsnGln 260
 DB 721 GGACTGATTAGAGAAATATAAGATCAATTTGTATAACATTTCTATAACCCAGGGTTTAAATCAA 780
 QY 261 PheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAspMetThr 280
 DB 781 TTTAATCGCTCAAAATGCTCAAGATTGGGTGAGCTTTAATAGGTTTCGTACAGATATGACA 840
 QY 281 LeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyrProLeu 300
 DB 841 TTAACAGTATTAGATCTCGCAATATTATTTCCAACTATGATCCACGTAGGTATCCATTA 900
 QY 301 AlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThrGlyVal 320
 DB 901 GCAGTAAAAACGGAAATTGACTAGGGAAGTTTATACAGATCCAGTAGGGTTTACTGGGTA 960
 QY 321 LeuGluSerGlyGlyArgThrTyrProTyrIleAsnProAsnAsnThrThrPheThrAla 340
 DB 961 TTGAAAAGTGAGGTAGGACTTACCCCTGGTATTAATCTCTAATAATACAACTTTTACTGCT 1020
 QY 341 MetGluAsnAsnAlaArgArgProSerTyrThrThrTyrTrpLeuAsnArgIlePheVal 360
 DB 1021 ATGGAAAATAACGCAGACGAGCTCCTTCTTATACCACCTTGGCTTAATCGTATTTTCTGA 1080
 QY 361 TyrThrArgThrLeuGlyAsnMetSerAspValArgAsnIleTyrPheGlyHisThrLeu 380
 DB 1081 TATACAGAGCTCTAGGTAAATATGCTGATGTGAGAAATATTTGGGAGGGGCATACATTA 1140
 QY 381 ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyLysThrAspSerIle 400
 DB 1141 GTTGAATAATGGAAATGATGGTTCTCGAAATAAACCATTAACCTTTGGTAAACATGATTCAT 1200
 QY 401 ThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIleGluSerLeuAla 420
 DB 1201 ACTCTATTCATATTATTTAATTTTCGGNACCTTTCTGTTTTTTCAGTATTGAGTCACTGCT 1260
 QY 421 ArgIleTyrLeuGlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSer 440
 DB 1261 CGTATATATTAGGAGAAACAGAGGCTAAATAATATATATTACTAGTCACTAGTGGAGTCTCG 1320
 QY 441 ArgValIlePheAsnThrSerAsnIleAsnAsnValProGlySerLeuArgTyrGluVal 460
 DB 1321 AGAGTATTTTAAATACATCAATTAATAATATGATCTGGATCTTTTAAGATACCAAGTG 1380
 QY 461 ProAlaAsnLeuProSerGlnThrIleLeuSerGluLeuProGlyLysAspLysProArg 480

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Db 1381 CTGCTAATCTTCCATCCCAAACTATATATATACAGAAATACCAAGAAAGTAAGCAAGA 1440
Qy 481 ProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArg 500
Db 1441 CCAACGCGAGGAGATTTCAGCCATAGATATATCTTATATATCAAAATTTTGATGCACGGCA 1500
Qy 501 SerSerSerGlyGlyIleValSerLeuThrPheGlyTyrPalaHisThrSerMetAsp 520
Db 1501 AGTAGTTACGGGGTATTGTTAGTCTTTTAAAGCTTTGGTGGGCACATACCAAGTATGGAT 1560
Qy 521 ArgAsnAsnArgLeuGlnProAspPheIleThrGlnIleAspAlaValIleGlyTyrGly 540
Db 1561 CGTAATAATCGCTTGAACCATGATAAAATTTCTCAAAATAGATGCAAGTTAAAGGTTGGGG 1620
Qy 541 GlyAsnIleGlyPheValIleProGlyProThrGlyGlyAsnLeuValIleSerAsp 560
Db 1621 GGGATATCGGCTTGTCTATCCAGGACCTACTGGGGGAATTTGGTAAAGTCAAGTAT 1680
Qy 561 SerTyrHisSerLeuIleValGlnAlaProGlnArgGlnThrSerTyrArgIleArgLeu 580
Db 1681 AGTTGGCATTCATTAAAGTTCAAGCACCACCAAGACAAACAAGTTATCGTATTCGTTT 1740
Qy 581 ArgTyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHisSerGlySerSer 600
Db 1741 CTTATGCTGTGTTAGTTACCCATGGGATGCTATTTTTGTAGAACACACAGCGCGAGTAGT 1800
Qy 601 HisIleValSerPheAspCysSerAsnSerSerGlyArgProSerAsnThrLeuLeu 620
Db 1801 CATATAGTTTCATTTTGTGCTCAATTCATCAGGTGCTCCATCAACACTTTCTA 1860
Qy 621 GluSerAspPheArgTyrIleAspValProGlyIlePheThrProSerIleAsnProLeu 640
Db 1861 GAGAGTGATTTTCGTATATTGATGTTCCAGGTATTTTACACCATCAATAATCCCTTA 1920
Qy 641 IleArgTyrArgThrGlnSerPheGlyThrHisAlaIleAspIlePheGluPheIlePro 660
Db 1921 ATAGATATAGAACCAAAAGCTTTGGTACCCACGCGATAGACAAATTTGAATTTATCCA 1980
Qy 661 LeuAsnThrPheProAsnGlnSerLeuGluIleValArgGluGlnValAsnAspLeuPhe 680
Db 1981 CTTACACTTTTCGAAATCAATCATTAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAG 2040
Qy 681 IleAsn 682
Db 2041 ATCAAT 2046
RESULT 2
ADR89409
ID ADR89409 standard; cDNA; 2016 BP.
XX
AC ADR89409;
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-009 alternative start site coding sequence.
XX
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 1..2016
FT /*tag= a
FT /product= "Alternative AXMI-009"
XX
PN WO2004074462-A2.
XX
PD 02-SEP-2004.
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PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 19-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783117.
XX
PA (ATHE-) ATHENIX CORP.
XX
PI Carozzi N, Hargies T, Korziel MG, Duck NB, Carr B;
XX
WPI; 2004-635574/61.
DR P-PSDB; ADR89410.
XX
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Claim 1; SEQ ID NO 21; 178pp; English.
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 2016 BP; 668 A; 315 C; 400 G; 633 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 2016
Score: 3536.00 Matches: 671
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 98.3% Indels: 0
DB: 13 Gaps: 0
US-10-782-096-2 (1-682) x ADR89409 (1-2016)
Qy 12 MetLeuAspAlaLeuArgIleAsnSerAsnMetSerAsnCysTyrProArgTyrProLeu 31
Db 1 ATGTTGGATGCTTTACGAATCAACTCTAATATGCTAATTTGTTATCCAAAGGTATCCACTA 60
Qy 32 AlalysAspProGlnMetThrMetArgAsnThrAsnTyrLysGluTyrLeuAsnMetCys 51
Db 61 GCAAAAGATCCACAAATGACTATGCGAAACACGAACTATAAAGATGGCTAAATATGTGT 120
Qy 52 AspSerAsnThrGlnPheIleGlyAspIleSerThrTyrSerSerProGluAlaAlaLeu 71
Db 121 GATTCAAATACACAAATTTATTTGGTGATATAGACGATATTCAGCCCTGAGCTGCTTTA 180
Qy 72 SerValArgAspAlaValLeuThrGlyIleAsnSerValGlyThrIleLeuSerAsnLeu 91
Db 181 AGTGACGAGATGCTGTTTAAACGGGTATTAAACAGTGTAGGACTATATCTTCGAATTTA 240
Qy 92 GlyValProLeuAlaSerGlnSerPheGlyIleIleSerArgLeuIleGlyIleLeuTyr 111
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|||||
1381 AACGACGAGATTTTCAGCCATAGATTATCTTATATCAAAATTTTGATGACGGCGAAGT 1440
QY SerSerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArg 521
|||||
1441 AGTTTCAGGCGGTATTTGTTAGTCTTTTAACGTTTGGTTGGCCACATACCAGTATGGATCGT 1500
QY AenAenArgLeuGluProAspValIleThrGlnIleAspAlaValIleGlyTrpGlyGly 541
|||||
1501 AATAATCGTCTTGAACACAGATAAATTACTCAAAATAGATGCGAGTTAAAGTTTGGGGGGG 1560
QY AenIleGlyPheValIleProGlyProThrGlyGlyAsnLeuValIleValSerAspSer 561
|||||
1561 AATATCGGGTTTGTATCCAGGACCTACTCGGGGGGAATTTTGGTAAAGTCAAGTATAGT 1620
QY TrpHisSerLeuIleValGlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArg 581
|||||
1621 TGGCATTTCACCTTAAAGTTTCAAGCACCACAAAGACAAACAAAGTTATCGTATTCGTTGGCT 1680
QY TyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHisSerGlySerHis 601
|||||
1681 TATGCTTGTAGTTTACCCTATGGGATGCTATTTTGTAGAACACAGCGCGAGTATGATCAT 1740
QY IleValSerPhePheAspCysSerAenSerSerGlyArgProSerAsnThrLeuLeuGlu 621
|||||
1741 ATAGTTTCATTTTGTGATTGCTCAATTCATCAGGTCGTCCATCAACACATCTCTAGAG 1800
QY SerAspPheArgTyrIleAspValProGlyIlePheThrProSerIleAsnProLeuIle 641
|||||
1801 AGTGATTTTCGTATATATTGATGTTCCAGGTATTTTACACCATCAATAAATCCCTTAATA 1860
QY ArgTyrArgThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeu 661
|||||
1861 AGATATAGAACACAAAGCTTTTGGTACCCACGCGATAGACAAATTTGAATTTTATCCACTT 1920
QY AenThrPheProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
|||||
1921 AACACTTTTCCGAATCAATCATTAGAAAAAGAGAACAGAGTAAATGATCATTTATTC 1980
QY Aen 682
|||||
1981 AAT 1983

RESULT 4
ABK87234
ID ABK87234 standard; DNA; 3621 BP.
XX
AC ABK87234;
XX
DT 07-OCT-2002 (first entry)
XX
DE Bacillus thuringiensis Cry1218-1 gene sequence.
XX
KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
KW insect target range; endotoxin; Cry1218; gene; ds.
XX
OS Bacillus thuringiensis.
XX
PN WO200234774-A2.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-US045468.
XX
PR 24-OCT-2000; 2000US-0242838P.
XX
PR 23-OCT-2001; 2001US-00032717.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LB;
XX
WPI; 2002-519178/55.

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DR P-PSDB; AAU99255.
XX
PT New isolated pesticidal polypeptide useful for impacting insect pest e.g.
PT Colorado potato beetle.
XX
PS Claim 1; Page 91-96; 176pp; English.
XX
CC The present invention relates to a new pesticidal polypeptide. The
CC invention is useful for impacting an insect pest by applying the
CC molecules of the invention to the environment of the insect pest by
CC spraying, dusting, broadcasting, or seed coating, where the insect pest
CC is selected from Colorado potato beetle, western corn rootworm or
CC southern corn rootworm. The invention is also useful for increasing
CC insect target range and for producing transgenic microorganisms and
CC plants that express the pesticidal polypeptide. The invention is also
CC useful for producing transformed plants and in transforming any organism
CC to produce the pesticidal polypeptide of the invention. The present
CC nucleic acid sequence encodes a Bacillus thuringiensis wild-type Cry1218
CC endotoxin protein
XX
SQ Sequence 3621 BP; 1277 A; 608 C; 771 G; 965 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.61e-77 Length: 3621
Score: 948.00 Matches: 248
Percent Similarity: 50.9% Conservative: 119
Best Local Similarity: 34.4% Mismatches: 276
Query Match: 26.4% Indels: 78
DB: 6 Gaps: 25

US-10-782-096-2 (1-682) x ABK87234 (1-3621)
QY 3 SerTyrLysAenLysAenGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
DB 4 AGTCAATAATCAAAATGAATATGAATATATAGATCGACACCT---TCTATTTCTGTA 60
QY 23 SerAenCysTyrProAspGlyTyrProLeuAlaLysAspProGlnMetThrMetArgAenThr 42
DB 61 TCCATGATTTCTAACAGATACCTTTTGGATGAGCCACAAATGCGCTACAAATATG 120
QY 43 AenTyrLysGluTrpLeuAsnMetCysAspSerAenThrGlnPheIleGlyAspIleSer 62
DB 121 GATTATTAAGATTTATTAATAATGTCT-----GCGGGAATGCTAGT 162
QY 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
DB 163 GAATACCTCGTTCACCTGAAAGTACTGTTTACGCGACAAGATGCAAGCTTAAGGCCCAAT 222
QY 82 AenSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
DB 223 GATATAGTAGTAATAATTACTATCAGTTTAGGGTCCCATTTTGTGGCCGATAGTAGT 282
QY 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
DB 283 CTTTATACTCAACTTATTTGATATCTGTGGCTTCAGGGGAAAAGAGTCAATGGGAAT 342
QY 120 LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAen 139
DB 343 TTTATGGAAACAGTAGAAGAACTCATTAATCAAAAATAGCAGAAATAGCAAGGAATAA 402
QY 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
DB 403 GCGCTTTCCGGAATTAGAGGATTAGGTAAATAATTACCAATTTATATCTAACTCGCTGAA 462
QY 160 AlaTrpLeuValAenLysAenAspAenArg---ArgAlaLeuValThrGlnTyrAla 178
DB 463 GAATGGGAAGAAATCCAAATGGTTCAAGAGCCTTACGAGATGTCGGAATCGATTTGAA 522
QY 179 IleValAspAenPheGluLysAsnMetProLysPheLysGluArgAspPheGluIle 198
DB 523 ATCTGGATGATTTTATTTACGCAATATATGCAATCTTTTAGAGTGACAAATTTTGAAGTA 582
QY 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAenLeuHisLeuLeuLeuArgAspAla 218

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Db 1768 GATATTGATGCTAAGATGCTCAGATTGAG-----ATGCCAAAA 1812
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 1813 ACAATGAACCGAGTGAGATCTGACATCTTAAACCTTTTAAAGTTGCAGATGCTATCACA 1872
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 1873 ACATTAAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATAAATTTAGGTGAAGACCTT 1932
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 1933 AATTCACAAATATCTCGTATAGTTTACGTTGACCGGAATCGAATTCATCCAGTAGATGAG 1992
Qy 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
Db 1993 ACATATGAAGCGCAACAGATTAGAACGACGAGCAAGACAGTGAATCCCTTGTTCAG 2052
Qy 682 Asn 682
Db 2053 AAT 2055
RESULT 6
AEB45606
ID AEB45606 standard; DNA; 3621 BP.
XX AC AEB45606;
XX 22-SEP-2005 (first entry)
DT B. thuringiensis Cry toxin, Cry1218-1 DNA.
XX DE Toxin; ds; gene; transgenic plant; insecticide; pesticide;
XX KW plant insect pest; Cry8.
XX OS Bacillus thuringiensis; strain 1218-1.
XX PN WO2005066349-A2.
XX PD 21-JUL-2005.
XX PF 09-DEC-2004; 2004WO-US041530.
XX PR 24-DEC-2003; 2003US-00746914.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Abad A, Dong H, Herzmann R, Lu A, Mccutchen BF, Rice JA;
PI Schepers EJ, Wong JF;
XX WPI: 2005-533612/54.
XX P-PSDB; AEB45607.
XX
PT Novel isolated nucleic acid molecule having nucleotide sequence encoding
PT pesticidal polypeptide comprising engineered proteolytic protection site
PT resistant to protease, useful for protecting plant from pest e.g.
PT Colorado potato beetle.
XX
PS Example 4; SEQ ID NO 1; 362pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
XX nucleotide sequence encoding a pesticidal polypeptide having an
XX engineered proteolytic protection site, which is not sensitive to the
XX plant protease and protects the pesticidal polypeptide from proteolytic
XX inactivation in a plant. Also included are protecting (M1) a pesticidal
XX polypeptide from proteolytic inactivation in a plant (comprising altering
XX a proteolytic site within the pesticidal polypeptide that is sensitive to
XX a plant protease to comprise a proteolytic protection site, where the
XX proteolytic protection site is not sensitive to the plant protease and
XX protects the pesticidal polypeptide from proteolytic inactivation in a
XX plant), an expression/cassette (II) comprising the nucleic acid, a

CC transformed plant (III) a stably incorporated with the expression
CC cassette in its genome, a transformed seed of the plant and an isolated
CC pesticidal polypeptide (IV) having proteolytic activity (and comprising
CC an engineered proteolytic protection site, which is not sensitive to the
CC plant protease and protects the pesticidal polypeptide from proteolytic
CC inactivation in a plant). The pesticidal polypeptide is Cry8Bb1 toxin or
CC its variant or fragment, where the variant and the fragment have
CC pesticidal activity and the variant has at least 70 % sequence identity
CC to an amino acid sequence for the Cry8Bb1 toxin. The nucleic acid and/or
CC expression cassette are useful for protecting a plant from a pest, where
CC produces the pesticidal polypeptide in the plant, and where the
CC pesticidal polypeptide protects the plant from the pest. The plant
CC protease is a cysteine protease. The pest is chosen from Colorado potato
CC beetle, Western corn rootworm, Southern corn rootworm, and boll weevil.
CC The present sequence encodes a wild-type Bacillus thuringiensis Cry8-like
CC toxin.
XX
SQ Sequence 3621 BP; 1277 A; 608 C; 771 G; 965 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3-61e-77 Length: 3621
Score: 948.00 Matches: 248
Percent Similarity: 50.9% Conservative: 119
Best Local Similarity: 34.4% Mismatches: 276
Query Match: 26.4% Indels: 78
DB: 14 Gaps: 25

US-10-782-096-2 (1-682) x AEB45606 (1-3621)
Qy 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 4 AGTCCAAATTAATCAAAATGAATATGAATATATAGATGCGACACCT---TCTACTTCTGTA 60
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 61 TCCATGATCTTAACAGATACCCCTTTTGGCAATAGCCCAACAAATCGCTACAAAATATG 120
Qy 43 AsnTyrLysGluTyrLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 121 GATTATAAGATTATTATAAATGCT-----GCGGGAATGCTAGT 162
Qy 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 163 GAATACCCCTGTTCACTGAGTACTTGTAGCGACAGATGTCAGTAAAGCGCGCAATT 222
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 223 GATATAGTAGGTAATTAATCTATCAGGTTAGGGGTCCTTTGTTGGCGCGATAGTGAGT 282
Qy 102 IleIleSerArgLeuIleGlyIleLeuTyrAlaGlyProAsp-----ProPheGluAla 119
Db 283 CTTTATCTCAACTTATTGATATTCTGTGGCCTTCAGGGGAAAAGAGTCAATCGGAATT 342
Qy 120 LeuMetValLeuValGluLeuIleLysSerIleAspGlnArgValArgGluAsn 139
Db 343 TTTATGGAACAGTAGAAGAACTTATTAATCAAAAATAGCAGATATCAAGGAATAAA 402
Qy 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 403 GCGCTTTCCGAATTAGAGGATTAGTAATAATTAATTAATTAATTAATTAATTAATTAAT 462
Qy 160 AlaTyrLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
Db 463 GAATGGGAAGAAATCCAAATGTTCAAGAGCTTACGAGATGTGCGAAATCGATTGAA 522
Qy 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
Db 523 ATCTCGTAGTATTATTATTCAGCAATATATGCTATCTTTAGAGTGCACAAATTTTGAAGTA 582
Qy 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
Db 583 CCATTCCTTACTGTATATGCAATGGCAGCAACCTTCAATTTTACTTGTATTAAAGGACGCG 642

QY 219 AspTyrPheGlyValAlaGlnTrpGlnLeuGlyAspAspGluLeuArgAspAsnTyrIleArg 238
Db 643 TCMAATTTTGGAGAAGATGGGGATGGTCAACAACACTATTATAAATCACTATTATGATCGT 702
QY 239 LeuGlnGlyLeuIleArgGluTyrIleAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 703 CAAATGAACCTTACTGCAGAAATATTCTGATCATCTGTGTAACCTGGTATGAACCTGGTTTA 762
QY 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
Db 763 GC AAAATTAAGAGCAGCAGCGCTAAACAATGGGTGACTATAACAATTCGGTAGAGAA 822
QY 279 MetThrLeuThrValIleAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 823 ATGACACTGGCGGTTTATGATGTTGTTCATTTATTCCTCCCAATATATACACACGACGCTAC 882
QY 299 ProLeuAlaValIleThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
Db 883 CCAATGGAAACGAAAGCAACAATAACAGGGAAGTATATACAGATCCACTGGCGCGGTA 942
QY 319 GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338
Db 943 AACGTGCTTCAATGGTTCC-----TGGTATGAC---AAAGCACCTTCTTTC 987
QY 339 ThrAlaMetGluAsnAlaArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
Db 988 GGAGTGATAGATCATCTCGTTTATTCGACCACCCCATGTATTGTGATTATATACGGGACTC 1047
QY 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
Db 1048 ACAGTGTATACAACTCAAGAGCATTTCTCCGCTCGCTATATAAGACAT---TGGGCT 1104
QY 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
Db 1105 GGTCACTAAATAAGTACCATCGTGTGCTAGTAGGGGTAGTAATCTTCAACAAATGTATGA 1164
QY 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
Db 1165 ACTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATTTATGATATTATACAG 1224
QY 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
Db 1225 ACTCTATCAAGAGTGCAGTACTCTTGATATTGTTTACCTCGTTTATAG----- 1275
QY 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
Db 1276 ---TATATATTT-----TTTGGATGCCAGAAGTCGAGTTTTTCATGGTAAACCAATG 1326
QY 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
Db 1327 AATAATACGAAGACGTTAAAGTAT-----AATCCAGTTTCCAAAGATATT 1374
QY 470 LeuSer-----GluLeuProGlyLysAspLysProArgProAsn 482
Db 1375 ATAGCGAGTACAAGAGATTCGGAATTAGAAATTTACTCCAGAAGCTTCAGATCAACCAAT 1434
QY 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgSerSer 502
Db 1435 TATGAGTCATATAGCCATAGATTATGTATATATATATATATATATATATATATATATAT 1494
QY 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn 522
Db 1495 ACCGGATTAGTACCT-----GTATTTTCTTGGACACATCGCAAGTGCAGATTTAAAC 1545
QY 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn 542
Db 1546 AATACAATATATTCAGATAAATCACTCAAAATTCGGCGGTAAATGTGG---GATAAT 1602
QY 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValIle 558
Db 1603 TTACCGTTTGTTCAGTGGTAAAGGACCCAGGACATACAGGAGGGGATTTATTACAGTAT 1662

QY 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
Db 1663 AATAGAACTACTGGTTCCTGTAGAACCTTATTCTAGCTCGATATGGCTAGCATTAGAA 1722
QY 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 1723 AAAGCAGGGAATATATCGTGAAGACTGAGATATGCTACT-----GATGCA 1767
QY 592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
Db 1768 GATATTGTATTGCTATGTAACCATGCTCAGATTTCAG-----ATGCCAAA 1812
QY 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 1813 ACAATGAACCCAGGTGAGGATCTGCATCTAAACTTTTAAAGTTGCAGATGCTATCACA 1872
QY 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 1873 ACATTAAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATAATTATTAGTTGAAGACCT 1932
QY 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 1933 AATTCAACATTTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTAGTAG 1992
QY 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
Db 1993 ACATATGAACGGACAAAGATTAGACAGCGGAAGAAAGCGATGCTTGTGTTAGC 2052
QY 682 Asn 682
Db 2053 AAT 2055
RESULT 7
AEB34684
ID AEB34684 standard; DNA; 3621 BP.
XX AEB34684;
XX
XX 22-SEP-2005 (first entry)
DE Bacillus thuringiensis Cry8Bb1 protoxin DNA.
XX
XX Plant insect pest; toxin; Cry8Bb1 protoxin; insecticide; pesticide; ds.
OS Bacillus thuringiensis.
XX
XX WO2005063996-A2.
PD 14-JUL-2005.
XX
XX 20-DEC-2004; 2004WO-US042736.
XX
XX 23-DEC-2003; 2003US-0532185P.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Abad A, Flannagan RD, Herrmann R, Lu A, Mccutchen BF;
PI Presnail JK, Rice JA, Wong JF, Yu C;
XX
XX WPI; 2005-541825/55.
XX
XX Protection of plants from insect pests comprises the introduction of a
PT polynucleotide construct that comprises a nucleotide sequence encoding an
PT insect protoxin; and cleavage of the protoxin by plant protease to form
PT active insect toxin.
XX
XX Example 1; SEQ ID NO 5; 65pp; English.
XX
XX The invention relates to a method of protecting a plant from an insect
CC pest comprising introducing a polynucleotide construct that comprises a
CC nucleotide sequence encoding an insect protoxin, operably linked to a
CC promoter that drives expression in the plant, where the insect protoxin

CC has at least one proteolytic activation site that has been engineered to
 CC comprise a cleavage site that is sensitive to a plant protease (within
 CC the plant), where expression of the construct produces the insect
 CC protoxin in the plant, where cleavage of the protoxin by a plant protease
 CC produces an active insect toxin and where the active insect toxin
 CC protects the plant from the insect pest. The invention also relates to an
 CC isolated nucleic acid molecule comprising a nucleotide sequence encoding
 CC the insect protoxin, an isolated nucleic acid molecule comprising a
 CC nucleotide sequence encoding a Cry8-like insect protoxin, impacting an
 CC insect pest of a plant comprising providing a transgenic plant that
 CC comprises in its genome a stably incorporated polynucleotide construct
 CC and a composition comprising at least one insect protoxin in combination
 CC with a carrier. The composition is useful for impacting insect pests
 CC (e.g. Colorado potato beetle, western corn rootworm, southern corn
 CC rootworm or boll weevil) on plants (e.g. monocot (maize) or dicot). The
 CC modified insect toxins (pro toxin forms of pesticidal polypeptides in
 CC conjunction with endogenous plant or insect gut proteases) are effective
 CC in pest management strategies. This sequence represents *Bacillus*
 CC *thuringiensis* Cry8Bb1 protoxin DNA of the invention.

XX
 SQ Sequence 3621 BP; 1277 A; 608 C; 771 G; 965 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3,61e-77	Length:	3621
Score:	948.00	Matches:	248
Percent Similarity:	50.9%	Conservative:	119
Best Local Similarity:	34.4%	Mismatches:	276
Query Match:	26.4%	Indels:	78
DB:	14	Gaps:	25

US-10-782-096-2 (1-682) x AEB34684 (1-3621)

QY	3	SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet	22
DB	4	AGTCCAAATATCAAAATGAATATGAATATAGATCGCACCT---TCTACTTCTGTA	60
QY	23	SerAsnCytyP:ProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr	42
DB	61	TCCAAATGATCTTAACAGATACCCCTTTTGGCAATGAGCCCAAAATGCGCTACAAAATATG	120
QY	43	AsnTyrLysGluTyrLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer	62
DB	121	GATTATAAGATTAATTTAAATATGCT-----GCGGGAATGCTAGT	162
QY	63	ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle	81
DB	163	GAATACCCCTGGTTCACCTGAGTACTTGTAGCGGACAGATGCAGCTAAGGCCCAATT	222
QY	82	AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly	101
DB	223	GATATAGTAGGTAATTAATCTATCAGGTTTAGGGTCCCATTTTGGGCGGATAGTAGT	282
QY	102	IleIleSerArgLeuIleGlyIleLeuTyrAlaGlyProAsp-----ProPheGluAla	119
DB	283	CTTTATACTCAACTTATTGATATTCTGTGGCTTCAGGGGAAGAGTAGTCAATGGGAATT	342
QY	120	LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn	139
DB	343	TTTATGGACAGTAGTAGAAGACTCATTAATCAAAAATAGCAGATATCAAGGATATAA	402
QY	140	AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgTyrGlnThrArgLeuGln	159
DB	403	CGCGTTTCGGAAATTAGAGGATAGGTAATAATTACCAATTATATCTAATCGCGTTGAA	462
QY	160	AlaTyrLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla	178
DB	463	GAATGGGAAGAAATCCAAATGGTTCAAGAGCCTTACAGAGATGTGCGAAATCGATTGAA	522
QY	179	IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle	198
DB	523	ATCTCGGATAGTTATTTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGA	582
QY	199	LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla	218

DB	583	COATTCCTTACGTGTATGCAATGGCAGCCAACTTCATTATTGTATTAAAGGACGG	642
QY	219	AspTyrPheGlyAlaGlnTyrGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg	238
DB	643	TCAATTTTGGAGAAGATGGGGATGGTCAACACTACTATTATAACTATTATGATCGT	702
QY	239	LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu	258
DB	703	CAATGAAATCTACTGCAGATATTCTGTATCACTGTGTAAAGTGGTATGAACTGGTTA	762
QY	259	AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp	278
DB	763	GCAAAATTTAAAGGACGAGCCCTAAACAAATGGGTGACTATAACCAATTCOGTAGAA	822
QY	279	MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr	298
DB	823	ATGACACTGGCGGTTTGTAGATGTTTGTGCAATTATTTCCCAATATTATGACACACG	882
QY	299	ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr	318
DB	883	CCAATGGAAACGAAAGCACACTAACAGGGAAGTATATACAGATCCACTGGGCGGTA	942
QY	319	GlyValLeuGluSerGlyGlyArgThrTyrProTyrPyrAsnProAsnAsnThrThrPhe	338
DB	943	AACGTGCTCTCAATTTGGTTCC-----TGGTATGAC---AAAGCACCTCTCTTTC	987
QY	339	ThrAlaMetGluAsnAsnAlaArgArgProSerTyrThrTyrTrpLeuAsnArgIle	358
DB	988	GGAGTGATAGAAATCATCCGTTATTCACCCACCCCTGATTTGATTTATTAACGGGACTC	1047
QY	359	PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTyrGly	376
DB	1048	ACAGTGTATACACAATCAAGAAGCATTTCTCCGCTCGCTATATATAAGACAT---TGGGCT	1104
QY	377	GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly	395
DB	1105	GGTCATCAAAATAGCTACCATCGTGTAGTGGGGTAGTAATCTTCAACAAATGTATGGA	1164
QY	396	LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer	415
DB	1165	ACTAATCAAAATCTACACAGCACTAGTACCTTTTGATTTTACGATTTATATTTACAAG	1224
QY	416	IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn	430
DB	1225	ACTCTATCAAGGATGCAGTACTCTTGATATTGTTTACCTGGTTATACG-----	1275
QY	431	AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle	449
DB	1276	---TATATATTT---TTTGGAAATGCCAGAAGTCGAGTTTTTCATGTTAAACCAATTG	1326
QY	450	AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle	469
DB	1327	ATAATATACCAGAAAGCGTTAAAGTAT-----AATCCAGTTTCCAAAGATATT	1374
QY	470	LeuSer-----GluLeuProGlyLysAspLysProArgProAsn	482
DB	1375	ATAGCGAGTACAAGAGATTTCGGAATTAGAAATTTACCTCCAGAAATTCAGATCAACCAAT	1434
QY	483	AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgSerSer	502
DB	1435	TATAGTCATATAGCCATAGATTATGTCATATACAAAGTATTCCCGCGAGCGGTAACT	1494
QY	503	SerGlyGlyIleValSerLeuLeuThrPheGlyTyrAlaHisSerMetAspArgAsn	522
DB	1495	ACCGGATTAGTACCT-----GTAATTTCTTGGACACATCGAAGTCGAGATTTAAAC	1545
QY	523	AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyGlyAsn	542
DB	1546	ANTACAATATATTACAGATAAATCACTCAAAATTCGCGCGGTAAATGTTGG---GATAT	1602
QY	543	IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal	558

Db 1603 TTACCGTTTGTTCAGTGGTAAAGGACCAGGACATACAGGAGGGAGTTTATTACAGTAT 1662
Qy 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
Db 1663 AATGAAGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTTAGAA 1722
Qy 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 1723 AAAGCAGGGAATATCTGTAGACTGAGATATGCTACT-----GATGCA 1767
Qy 592 IlePheValGluHisSerGlySerSerHisIleValSerPheAspCysSerAsnSer 611
Db 1768 GATATTGTTATTCATGTAACGATGCTCAGATTTCAG-----ATGCCAAA 1812
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 1813 ACAATGAACCCAGGTGAGGATCTGATCATCTAAACCTTTTAAAGTTGTCAGATCTATCACA 1872
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 1873 ACATTAATTTAGCAACAGATAGTTGCTAGCATTTGAAACATAATTTAGTGAAGACCTT 1932
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 1933 AATTCAACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTAGATGAG 1992
Qy 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
Db 1993 ACATATGAAGCGGAAACAGATTTAGAACGAGCGAAGAAAGCAGTGAATGCCTTGTTTAGC 2052
Qy 682 Asn 682
Db 2053 AAT 2055

RESULT 8

ABK87247

ID ABK87247 standard; DNA; 4874 BP.

XX AC ABK87247;

XX DT 07-OCT-2002 (first entry)

XX DE Bacillus thuringiensis genomic Cry1218-1 DNA sequence.

XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
KW insect target range; endotoxin; Cry1218; gene; ds.
XX OS Bacillus thuringiensis.

XX FN WO200234774-A2.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-US045468.

XX PR 24-OCT-2000; 2000US-0242838P.

XX PR 23-OCT-2001; 2001US-00032717.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

XX DR WPI; 2002-519178/55.

XX PT New isolated pesticidal polypeptide useful for impacting insect pest e.g.
XX Colorado potato beetle.

XX PS Claim 13; Page 144-145; 176pp; English.

XX CC The present invention relates to a new pesticidal polypeptide. The
XX invention is useful for impacting an insect pest by applying the the
XX molecules of the invention to the environment of the insect pest by
CC spraying, dusting, broadcasting, or seed coating, where the insect pest
CC is selected from Colorado potato beetle, western corn rootworm or
CC southern corn rootworm. The invention is also useful for increasing and
CC insect target range and for producing transgenic microorganisms and
CC plants that express the pesticidal polypeptide. The invention is also
CC useful for producing transformed plants and in transgenic any organism
CC to produce the pesticidal polypeptide of the invention. The present
CC nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type Cry1218
CC endotoxin protein
XX SQ Sequence 4874 BP; 1707 A; 787 C; 1003 G; 1377 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 5,466-77 Length: 4874
Score: 948.00 Matches: 248
Percent Similarity: 50.9% Conservative: 119
Best Local Similarity: 34.4% Mismatches: 276
Query Match: 26.4% Indels: 78
DB: 6 Gaps: 25
US-10-782-096-2 (1-682) x ABK87247 (1-4874)
Qy 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 734 AGTCCAAATAATCAAAATGAATATGAAATTTATAGATGCGACACCT---TCTACTTCTGTA 790
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 791 TCCATGATTTCTAACAGATACCTCTTTTCGGAATGAGCCAAATATGCCCTACAAATATG 850
Qy 43 AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 851 GATTATAAAGATTATTTAAATGTCT-----GCCGGAATGCTAGT 892
Qy 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 893 GAATACCCCTGGTTTACCTGAACTACTTGTAGCGGACAAGATGCAAGTAAAGCCCAATT 952
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 953 GATATAGTAGGTAAATTAATCTATCAGTTTAGGGGTCCCATTTTGTGGCCGAGTAGT 1012
Qy 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
Db 1013 CTTTATATCTCACTTATTTGATATTTCTGGCTTCAGGGGAAAGAGTCAATGGGAATT 1072
Qy 120 LeuMetValLeuValGluLeuLeuLysSerIleAspGlnArgValArgGluAsn 139
Db 1073 TTTATGGAAACAAGTAGAAGAACTCATTAAATCAAAAAATAGCAGAAATATGCAAGGAATAA 1132
Qy 140 AlaLeuArgGluLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 159
Db 1133 GCGCTTTCGGAATTAGAAAGGATTAGGTAAATTAATTAACCAATTATATCTAATCGCTTGA 1192
Qy 160 AlaTrpLeuValAsnLysAsnAspAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
Db 1193 GAATGGGAAGAAATCCAAATGGTTCAAGACCTTACGAGATGTCGAAATCGATTGAA 1252
Qy 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
Db 1253 ATCTCGGATAGTTTATTTACGCAATATATGCAATCTTTTAGAGTGACAAAATTTTCAAGTA 1312
Qy 199 LeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
Db 1313 CCATTCCTTACTGTATATGCAATGCGACCAACCTTCATTTACTGTATTAAAGACGGC 1372
Qy 219 AspTyrPheGlyValGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
Db 1373 TCAATTTTGGAGAAGATGGGATGGTCAACACTACTATTAATACTATTATGATCGT 1432
Qy 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 1433 CAAATGAACCTTACTGCGAATATTTCTGATCATTCTGTAAAGTGTGATGAACTGTTTA 1492

Alignment Scores:

Pred. No.: 5,46e-77 Length: 4874
 Score: 948.00 Matches: 248
 Percent Similarity: 50.9% Conservative: 119
 Best Local Similarity: 34.4% Mismatches: 276
 Query Match: 26.4% Indels: 78
 DB: 12 Gaps: 25

US-10-782-096-2 (1-682) x ADL15320 (1-4874)

QY 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
 DB 734 AGTCAAAATATCAAAATGAATGAATATAGATGCGACACCT---TCTACTTCTGTA 790
 QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
 DB 791 TCCAATGATTTCAACAGATACCCCTTTTGGCAATGAGCCCAAAATGCGCTACAAAATATG 850
 QY 43 AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
 DB 851 GATTATTAAGATATTTAAATGCTCT-----GCCGGAATGCTAGT 892
 QY 63 ThrTyr---SerSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
 DB 893 GAATACCCCTGGTTCACTGAGTACTTGTAGCGGACAGATGCGACTAAGGCCGCAATT 952
 QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
 DB 953 GATATAGTAGTAAATTAATCACTCAGGTTTAGGGTCCCAATTTGTTGGCCGATAGTGAGT 1012
 QY 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
 DB 1013 CTTTATACCTCACTTATGATATTTCTGTCGCTTACGGGAAAAAGATCAATGGGAAT 1072
 QY 120 LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
 DB 1073 TTTATGGAACTAGTAACTCATTATCAAAATAATAGCAGAAATATGCAAGGAATAA 1132
 QY 140 AlaLeuArgGluLeuGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
 DB 1133 GCGCTTTCGGAATTAGAAGGATTAGGTAAATAATTAACCAATATATCTAACTCGCTGTA 1192
 QY 160 AlaTrpLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
 DB 1193 GAATGGGAAGAAATCCAAATGGTTCAAGAGCCTTACGAGATGTGCGAAATCGATTGAA 1252
 QY 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
 DB 1253 ATCCCTGGATAGTTATTTACGCAATATATGCCATCTTTAGAGTGACAAATTTTGAAGTA 1312
 QY 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
 DB 1313 CCATTCCTTACTGTATATGCAATGCGCAGCAACCTTCAATTTACTGTATTAAAGGACGG 1372
 QY 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
 DB 1373 TCAATTTTGGAGAAGATGGGGATGGTCAACACTACTATTAACTAATTAATGATCGT 1432
 QY 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
 DB 1433 CAATGAAACTTACTGCGCAATATTCTGTATCATCTGTGTAAAGTGGTATGAACTGGTTTA 1492
 QY 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
 DB 1493 GCAAAATTAAGGACGACGAGCTAAACAAATGGGTGACTATATAACCAATTTCCGTAGAGAA 1552
 QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
 DB 1553 ATGACACATGGCGGTTTATGATGTTGTGCAATTTATCCCAATTTATGACACGACGATAC 1612
 QY 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
 DB 1613 CCAATGGAAACGAAACCAACTAAACAGGGAAGTATATACAGATCCACTGGCGCGGTA 1672

QY GlyValLeuGluSerGlyGlyArgThrTyrProTyrPyrAsnProAsnAsnThrThrPhe 338
 DB 1673 AACGGTCTCTCAATTTGGTTCC-----TGGTAAGAC---AAAGACCTCTTCTTTC 1717
 QY ThrAlaMetGluAsnAsnAlaArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
 DB 1718 GGAGTGATAGAATCATCGTTATTTCGACCACCCCATGTATTGATTATATAACGGGACTC 1777
 QY PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
 DB 1778 ACAGTGATACACAACTCAAGAAGCATTTCTTCGCTCGCTATATAAGACAT---TGGGCT 1834
 QY GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
 DB 1835 GGTCAATAAATAGCTACCATCGTGTAGTGGGTAGTAACTTCITCAACAATATGATGGA 1894
 QY LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
 DB 1895 ACTAATCAAAATCTACACAGCAGCTAGTACCTTTGATTTTACGAATATGATATTTACAAG 1954
 QY IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
 DB 1955 ACTCTATCAAAAGGATGCGAGTACTCTCTGATATTTGTTTACCTCGTGTATACG--- 2005
 QY AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
 DB 2006 ---TATATATT---TTTGGAAATGCCAAGTCGAGTGTTCATGGTAAACCAATG 2056
 QY AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
 DB 2057 AATAATACCAGAAAGACGCTTAAAGTAT-----AATCCAGTTTCCAAGATATT 2104
 QY LeuSer-----GluLeuProGlyLysAspLysPheArgProAsn 482
 DB 2105 ATAGCGAGTACAAGAGATTCGGAATTAGAATTCCTCCAGAAACTTCAGATCAACCAAT 2164
 QY AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgSerSer 502
 DB 2165 TATAGTCATATAGCCATAGATATGTCTATACAGATATTCGCCGCGCGGTAACT 2224
 QY SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn 522
 DB 2225 ACCGGATTAGTACCT-----GTAATTTCTTGGACACATCGAAGTCAGATTTAAAC 2275
 QY AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyGlyAsn 542
 DB 2276 AATACAATATATTCAGATAAAATCACTCAAAATTCGCGCGCTTAAATGTGG---GATAAT 2332
 QY IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal 558
 DB 2332 TTACCGTTTGTTCAGTCGTGTAAGGACGAGCATACAGGAGGGGATTTATTACAGTAT 2392
 QY SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
 DB 2393 AATAGAGTACTGGTTCGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTAGAA 2452
 QY ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
 DB 2453 AAAGCAGGGAATAATTCGTGAAGACTGAGATATGCTACT-----GATGCA 2497
 QY IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
 DB 2498 GATATTGTATGCTAGTAAACGATGCTCAGATTTCAG-----ATGCCAAA 2542
 QY SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
 DB 2543 ACAATGAACCCAGGTGAGGATCTGACATCTAAACCTTTTAAAGTTGCGATGCTATCACA 2602
 QY IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
 DB 2603 ACATTAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATAATTTAGGTGAAGACCT 2662

Db 1493 GCAAAATTAAGGACGAGCGCTAAACAATGGGTGACTATATAACCAATTCGCTAGAGAA 1552
Qy 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgTyr 298
Db 1553 ATGACACTGGCGGTTTATAGATGTTGTGATTAATTCACCAAAATTATGACACAGCGCATAC 1612
Qy 299 ProLeuAlaValIleThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
Db 1613 CCAATGGAAACCAAGACCACTAACAGGGAAGTATATACAGATCCACTGGCGCGGTA 1672
Qy 319 GlyValLeuGluSerGlyGlyArgThrTyrProTyrTyrAsnProAsnAsnThrThrPhe 338
Db 1673 AACGTGCTCTCAATTGGTTCC-----TGGTATGAC-----AAAGCACCTTCTTTTC 1717
Qy 339 ThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrThrTrpLeuAsnArgile 358
Db 1718 GGAGTGATAGAAATCATCGTTTATTCGACCCCATGATTTTGATTTATATATAACGGGACTC 1777
Qy 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
Db 1778 ACAGTGTATACAACTCAAGAGCATTTCTCCGCTCGCTATATAAGACAT---TGGGCT 1834
Qy 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
Db 1835 CGTCATCAAAATAAGCTACCATCGTGTAGTAGGGGTAGTAATCTTCAACAATGTATGGA 1894
Qy 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
Db 1895 ACTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATTTATGATATTTTACAG 1954
Qy 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
Db 1955 ACTCTCATCAAGGATCGAGTACTCTTGATATTGTTTACCTCGTTATACG----- 2005
Qy 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
Db 2006 ---TATATATTT-----TTTGGAATGCCAGAAGTCGAGTGTTCATGCTAAACCAATG 2056
Qy 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
Db 2057 AATAATACCAAGAAACGCTTAAAGTAT-----AATCCAGTTTCCAAAGATATT 2104
Qy 470 LeuSer-----GluLeuProGlyLysAspLysProArgProAsn 482
Db 2105 ATAGCGAGTACAGAGATTCGGAATTAAGATTAATCTCCAGAACTTCAGATCAACCAAT 2164
Qy 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSer 502
Db 2165 TATGAGTCATATAGCCATAGATTATGTATATATACAAAGTATTCGCGCGAGGGAACACT 2224
Qy 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn 522
Db 2225 ACCGGATTAGTACCT-----GTATTTCTTGACACATCGAAGTGCAGATTTAAC 2275
Qy 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyGlyAsn 542
Db 2276 AATACATATATTTCAGATAAATCACTCAATTCGCGCGTTAAATGTGG---CATAT 2332
Qy 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal 558
Db 2333 TTACCGTTGTTCCAGTGTAAGGACCCAGGACATACAGAGGGGATTTATTACAGTAT 2392
Qy 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
Db 2393 AATAGAAGTACTGGTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCCTAGCATTTAGAA 2452
Qy 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 2453 AAAGCAGGGAATATCGTGTAGATCTGATGATGTACT-----GATGCA 2497
Qy 592 IlePheValGluHisSerGlySerHisIleValSerPhePheAspCysSerAsnSer 611
Db 2498 GATATTGTATTCATGTAAACGATGCTCAGATTTCAG-----ATGCCAAA 2542

Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 2543 ACATGAACCCAGGTGAGGATCTGCATCTAAAACCTTTTAAAGTTGCAGATGCTATCACA 2602
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 2603 ACATTAAATTTAGCAACACAGATAGTTGCTAGCATTTGAAACATAATTTAGGTGAAGACCCT 2662
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 2663 AATTCAACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCCATAGTAGATGAG 2722
Qy 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
Db 2723 ACATATGAGCGGAACAAGATTATAGACCAGGAAGACGATGATGCCTTGTATTACG 2782
Qy 682 Asn 682
Db 2783 AAT 2785
RESULT 11
AAT43221
ID AAT43221 standard; DNA; 3507 BP.
XX AAT43221;
XX AAT43221;
DT 16-OCT-2003 (revised)
DT 28-JAN-1997 (first entry)
XX
DE Antiscarab pest toxin 50C(b) coding sequence.
XX
KW Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;
KW larval stage insect; grain; tuberous crop; white grub; chafer grub;
KW cyclocephala; popillia; ds.
XX
OS Bacillus thuringiensis; strain kumamotoensis.
XX
PN US5554534-A.
XX
PD 10-SEP-1996.
XX
PF 30-SEP-1994; 94US-00315468.
XX
PR 16-DEC-1991; 91US-00808316.
PR 30-JAN-1992; 92US-00828430.
PR 01-FEB-1993; 93US-00014941.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Foncerrada L, Narva KE, Michaelis TE;
XX
XX WPI; 1996-424659/42.
DR P-PSDB; AAW06417.
XX
PT New nucleic acid encoding B.thuringiensis toxin active against scarab(s)
PT - also related toxin and transformed microbes, effective against adult
PT pests and their larvae.
XX
PS Claim 2; Col 27-30; 24pp; English.
XX
CC AAT43221-T43223 represent the coding sequences for toxins that are active
CC against scarab pests. This sequence was isolated from the Bacillus
CC thuringiensis strain kumamotoensis. Insects in the family Scarabaeidae
CC constitute a serious pest control problem, especially when destructive
CC larval stage insects infest high value turf found in golf courses,
CC playing fields and lawns. The larvae of many species also attack grains,
CC tuberous crops, and ornamentals. The larvae are known as white grubs, or
CC chafer grubs, and can be found in decaying organic matter, or in the soil
CC where they consume plant roots. In Europe and the U.S. populations of
CC these larvae and adults have developed resistance to chemical
CC insecticides such as the organochlorines and DDT. The toxins encoded by
CC these sequences, and intact cells that are capable of expressing the


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Db 1798 AACGACATATCTCAATAAATAATGAAATGATTTTAAACATATAATGATTTTCAAAATATATA 1857
Qy 628 AspValProGlyIlePheThrProSerIleAsnProLeuIleArgTyArgThrGlnSer 647
Db 1858 GAATATCCAAGAGTCATT-----TCAGTAAATGCTTCTTCAACATACAGAGGTTATCT 1911
Qy 648 PheGlyThrHisAla-----IleAspLysPheGluPheIleProLeu 661
Db 1912 ATAGGTATACAAACGAATACAAATTTATTTATTTAGACCGGAATCGAATTTATCCAGTA 1971
Qy 662 Asn-----ThrPheProAsnGlnSer---LeuGluLysArgGluGlnGluValAsnAspLeu 679
Db 1972 GATGACATATGAAGCGGAACGATTTAGAACGCGCAAGCAAGACAGTGAATCCCTTG 2031
Qy 680 PheIleAsn 682
Db 2032 TTTACGAAT 2040

RESULT 12
ABK51132
ID ABK51132 standard; cDNA; 3690 BP.
XX
AC XX
XX
XX 30-JUL-2002 (first entry)
XX
XX cDNA encoding Bacillus thuringiensis insecticidal protein.
DE
XX
XX Insecticide; transgenic; Coleoptera larvae; ss; gene.
XX
XX Bacillus thuringiensis.
XX
XX Key Location/Qualifiers
FT CDS 187..3690
FT /*tag= a
FT /product= "Insecticide protein"
XX
XX JP2002045186-A.
XX
XX 12-FEB-2002.
XX
XX 03-AUG-2000; 2000JP-00236140.
XX
XX 03-AUG-2000; 2000JP-00236140.
XX
XX (SDSB-) SDS BIOTECH CORP.
XX
XX WPI; 2002-356468/39.
XX
XX P-PSDB; AAU80281.
XX
XX A protein having insecticidal activity, a DNA encoding said protein, and
XX an agent and a method for preventing harmful organisms.
XX
XX Claim 4; Page 17-18; 19pp; Japanese.
XX
XX This invention relates to a crystalline protein comprising a fully
XX defined sequence and the nucleotide sequence encoding this protein. The
XX protein of the invention is an agent for preventing harmful organisms
XX comprising Bacillus thuringiensis serovar galleriae SDS502, its mutant or
XX a microbe transformed by a DNA encoding the protein. This microbe can be
XX used to produce a protein containing the protein, or containing a protein
XX having insecticidal activity produced by the SDS502, its mutant or a
XX transformed microbe, a microbe which is transformed by using the above
XX DNA and produces the above protein having insecticidal activity, a plant
XX or a seed transformed by using the above DNA, and Bacillus thuringiensis
XX serovar galleriae SDS502 producing a protein comprising and producing a
XX protein showing insecticidal activity. The protein of the invention may
XX have insecticidal activity. The agent is used for preventing Coleoptera
XX larvae. This sequence represents the cDNA encoding the Bacillus
XX thuringiensis insecticide protein of the invention
XX
XX Sequence 3690 BP; 1289 A; 599 C; 762 G; 1040 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.: 1-84e-76 Length: 3690
Score: 940.50 Matches: 256
Percent Similarity: 51.8% Conservative: 111
Best Local Similarity: 36.1% Mismatches: 288
Query Match: 26.1% Indels: 56
DB: 6 Gaps: 23

US-10-782-096-2 (1-682) x ABK51132 (1-3690)
Qy 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 190 AGTCCAAATAATCAAAATGAATATGAATTTCTAGATGCT---TCATCATCTACTTCTGTGA 246
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 247 TCCGATATTTCTGTGTAGATACCTTTAGCAAAACGATCAAAACGACCACATTTACAAACATG 306
Qy 43 AsnTyrLysGluTrpLeuAsnMetCysAsp---SerAsnThrGlnPheIleGlyAspIle 61
Db 307 AACTATATAAGATTATCTGAGAATGTCTGAGGAGAGAAATCTCTGAATTTATTTGGAAATCCG 366
Qy 62 SerThrTyrSerSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 367 GAGACGTTTATTAGT-----TCATCTACGGTTTCAAACTGGAATT 405
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 406 GGCATTGTGTGCTCAAGTACTGCGGGCTTTAGGGGTTCCATTTGCTGGACAGATAGCTAGT 465
Qy 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyPro-----AspProPheGluAla 119
Db 466 TTTTATAGTTTCATTGTGCGTCAATTTATGGCCATCAAGTACCGTGAGTGATGGGAATG 525
Qy 120 LeuMetValLeuValGluGluLeuIleLysSerIleAspGlnArgValArgGluAsn 139
Db 526 ATTATGAACAAGTGGAGATCTAATTGATCAAAAATAACAGATTTCTGTAAAGAAACA 585
Qy 140 AlaLeuArgGluLeuGluGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 586 GCGCTTGCAAGACTACAGGATTTAGGAGATGGCTTAGACGTATATATACGAAATACACTAAG 645
Qy 160 AlaTrpLeuValAsnLysAsnAspAsnArgAla---LeuValThrGlnTyrAla 178
Db 646 AATTGGCTGGAAATCGTAATGATACAGAGCTAGAAGTGTGTGGTGACCAATATATA 705
Qy 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
Db 706 GCTTTAGAGCTTGATTTTGTGTTGCTAAAATCCATCTTTTGCATATATCTGGACAGGA 765
Qy 199 LeuLeuLeuProValTyrAlaGlnAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
Db 766 CCATTATTATCAGTGTATGCACAAGCAGCGAATTTTACATTTGCTATTTATACGAGATGCT 825
Qy 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
Db 826 TCCATTTTGGACAGAGTGGGGATTCACACAGAGAGAAATTTCCACATTTTATGATCGT 885
Qy 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 886 CAGGTGACACGTCACGCCCAATCTCGGATTATTGTGTAAAGTGTGTAACACATGGCTTA 945
Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
Db 946 GATAAATTTAAAGGTACGAATGCTGCAAGTGGCTGAAGTATCAACCAATTCGGAAGAAA 1005
Qy 279 MetThrThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 1006 ATGACATTACTGGTATTAGATTAGTCGGTTATTTCCAAACTATATGACACAGTACGTAT 1065
Qy 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
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Db 4 AGTCCAAATAATCAAAATGAATATGAAATATAGATGCGACACCT---TCTACTTCTGTGTA 60
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 61 TCCAATGATTCTTAACACAGATACCTTTTGGCAATGAGCCCAAAATGCGCTACAAAATATG 120
Qy 43 AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 121 GATTATAAAGATATTATTAATAATGCT-----GCGGGAATGCTAGT 162
Qy 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 163 GAATACCTCGTGTACCTGAAGTACTTGTAGCGGACAAGATGACGTAAGGCCGCAATT 222
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 223 GATATAGTAGTAATATTACTACGTTTAGGGTCCCATTTGTTGGCCGATAGTAGT 282
Qy 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
Db 283 CTTTATATCTCAACTTATTGATATTCGTGGCCCTCAGGGGAAGAGTCATGGGAATTT 342
Qy 120 LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
Db 343 TTTATGGAAACAAGTAGAAGACTATTAAATCAAAAAATAGCAGATAATGCAAGGAATAAA 402
Qy 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 403 CGCTTTCCGGAATTAGAAGGATAGTGAATAATTAACCAATTATATCTAACTCGCGTTGAA 462
Qy 160 AlaTrpLeuValAsnLysAsnAspAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
Db 463 GAATGGGAAGAAATCCAAATGGTTCAGAGCCCTACAGAGCTGCGGAAATCGATTGAA 522
Qy 179 IleValAspAsnPheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
Db 523 ATCTCGGATAGTTTATTTAGGCAATATATGCCATCTTTTAGAGTGACAAATTTTCAAGTA 582
Qy 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHleLeuIleLeuLeuArgAspAla 218
Db 583 CCATTCCTTACTGTATATGCAATGCGAGCCACCTTCATTTACTGTTATTAAAGGACGCG 642
Qy 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
Db 643 TCAATTTTGGAGAAATGGGATGGTCAACAACTACTATTAACTATTATGATCGT 702
Qy 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 703 CAAATGAATCTTACTGCAGATATTCTGATCACTGTGTAAGTGTATGAACCTGGTTTA 762
Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
Db 763 GCAAAATTTAAAGGCGACGAGCGCTAAACAATGGGTGACTATTAACCAATTCGTTAGAGAA 822
Qy 279 MetThrLeuThrValIleuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 823 ATGACACTGGCGGTTTATAGTGTGTTGCAATTATTCCTCAATTTCCCAAAATTTACACACGACGTCAC 882
Qy 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
Db 883 CCAATGGAAACGAAAGCAACAATAACAGGGAAGTATATACAGATCCACTGGCGCGGTA 942
Qy 319 GlyValLeuGluSerGlyClyArgThrTyrProTrpTyrAsnProAsnAsnThrPhe 338
Db 943 AACGTGCTCTCAATTTGGTTCC-----TGGTATGAC---AAAGCACCTTCTTTC 987
Qy 339 ThrAlaMetGluAsnAsnAlaArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
Db 988 GGAGTAGATAGATTCCTCGTATTTCGACCCCACTGATTTTGTGATTATATACGGGACTC 1047
Qy 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
Db 1048 ACAGTGTATACAAATCAAGAAGCATTTCTTCGCTCGCTATATTAAGACAT---TGGGCT 1104

Qy 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
Db 1105 GGTCAATCAATAAGTACCATTCCGTGCTAGTAGGGGTAGTAATCTTCAACAATGTATGGA 1164
Qy 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
Db 1165 ACTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATATGATATTTACAAG 1224
Qy 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyThrGlyThrGluAlaAsn 430
Db 1225 ACTCTATCAAAAGGATGCGAGTACTCTCTGATATTGTTTACCCTGGTTATACG----- 1275
Qy 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
Db 1276 ---TATATATTT-----TTTGGAAATGCCAAGTCGAGTTTTTTCATGGTAAACCAATIG 1326
Qy 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
Db 1327 AATAATACCAGAAGACGTTAAAGTAT-----AATCCAGTTTCCAAAGATATT 1374
Qy 470 LeuSer-----GluLeuProGlyLysAspLysProArgProAsn 482
Db 1375 ATAGCGAGTACAGAGATTCGGAATTAGAATTACCTCCAGAACTTCAGATCAACCAAT 1434
Qy 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgSerSer 502
Db 1435 TATGAGTCATATAGCCATAGATTATGTCAATATCAAGATATTCGCCGACCGGTAACT 1494
Qy 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn 522
Db 1495 ACCGATTAGTACCT-----GTATTTCTTGGACACATCGAAGTCGAGATTTAAAC 1545
Qy 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn 542
Db 1546 AATACAATATATTCAGATAAAATCACTCAAAATTCGCGCGTTAAATGTTGG---GATAT 1602
Qy 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal 558
Db 1603 TTACCGTTTGTTCAGGTGTTAAAGGACGACATACAGGAGGGGATTTATTACAGTAT 1662
Qy 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
Db 1663 AATAGAGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTAGAA 1722
Qy 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 1723 AAAGCAGGGAATATCGTGAAGACTGAGATATGCTACT-----GATGCA 1767
Qy 592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
Db 1768 GATATTGTTGTCATGTAAACGATGCTCAGATTTCAG-----ATGCCAANA 1812
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 1813 ACAATGAACCCAGGTGAGGATCTGCATCTAAAACCTTTTAAAGTTGCAGATGCTATCACA 1872
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 1873 ACATTTAAATTTAGCAACACAGATAGTTGCTGCAATTTGAAACATATAATTTAGGTGAAGACCCT 1932
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn 662
Db 1933 AATTCACATTTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTAGAT 1989
RESULT 14
ASK87241
ID ASK87241 standard; DNA; 2010 BP.
XX
AC ASK87241;
XX
DT 07-OCT-2002 (first entry)
XX

DE Bacillus thuringiensis Cry1218-1A truncated gene sequence.

XX Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 KW insect target range; endotoxin; Cry1218; gene; ds.

XX Bacillus thuringiensis.

XX WO200234774-A2.

XX 02-MAY-2002.

XX 24-OCT-2001; 2001WO-US045468.

XX 24-OCT-2000; 2000US-0242838P.

XX 23-OCT-2001; 2001US-00032717.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
 P-PSDB; AAU99262.

XX WPI; 2002-519178/55.

XX P-PSDB; AAU99262.

XX New isolated pesticidal polypeptide useful for impacting insect pest e.g.
 PT Colorado potato beetle.

XX Claim 1; Page 123-125; 176pp; English.

XX The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the the
 CC molecules of the invention to the environment of the insect pest by
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transforming any organism
 CC to produce the pesticidal polypeptide of the invention. The present
 CC nucleic acid sequence encodes a Bacillus thuringiensis wild-type Cry1218
 CC endotoxin protein

XX SQ Sequence 2010 BP; 690 A; 348 C; 394 G; 578 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-74e-75	Length:	2010
Score:	926.00	Matches:	239
Percent Similarity:	50.8%	Conservatives:	116
Best Local Similarity:	34.2%	Mismatches:	268
Query Match:	25.7%	Indels:	76
DB:	6	Gaps:	23

US-10-782-096-2 (1-682) x ABK87241 (1-2010)

QY	3	SerTyrLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet	22
DB	4	AGTCCAAATAATCAAAATGAATATGAATATAGATGCGACACCT---TCTACTTCTGTA	60
QY	23	SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAnthr	42
DB	61	TCCAAATGATCTTAACAGATACCCCTTTTGGAAATGAGCCCAAAATGCGCTACAAAATATG	120
QY	43	AsnTyrLysGluTyrLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer	62
DB	121	GATTATTAAGATATTTAAATGCTCT-----GCGGAAATGCTAGT	162
QY	63	ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle	81
DB	163	GAATACCCCTGGTTACCTCAAGTACTTGTAGCGGACAGATGCGACTAAGCGCGCAATT	222
QY	82	AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly	101
DB	223	GATATAGTAGGTAATAATCTACTATCAGGTTTGGGGTCCCAATTTTGTGGCCGATAGT	282

QY	102	IleIleSerArgLeuIleGlyIleLeuTyrPAlaGlyProAsp-----ProPheGluAla	119
DB	283	CTTTATACTCAACTATTGATATTCTGTGGCCTTCAGGGGAAAAGAGTCAATGGGAATT	342
QY	120	LeuMetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn	139
DB	343	TTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAATAGCAGATATGCAAGGAATAA	402
QY	140	AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln	159
DB	403	GGCTTTTCGAATTAGAGATTAGTAATAATTACCAATTATATCTAATCGCTTGA	462
QY	160	AlaTyrLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla	178
DB	463	GAATGGGAGAAAATCCAAATGGTTCAGAGAGCTTACGAGATGTGCGAAATCGATTGA	522
QY	179	IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle	198
DB	523	ATCTGGATAGTTTATTACGCAATATATATGCCATCTTTTAGAGTGCACAAATTTGA	582
QY	199	LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla	218
DB	583	CCATTCTTACTGTATATGCAATGCGAGCCCACTTCATTACTGTATTAAAGGACGCG	642
QY	219	AspTyrPheGlyAlaGlnTyrGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg	238
DB	643	TCAATTTTGGAGAAAGATGGGGTGTCAACAACCTACTATTATAAATACTATTATGATCGT	702
QY	239	LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu	258
DB	703	CAAAATCAAACTTACTGCGAATAATTCTGTATCACTGTGTAAAGTGGTATGAAATCTGTTA	762
QY	259	AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp	278
DB	763	GCAAAATTAAGGCGCAGCGCTAAACATGGTGTGACTATACCAATTCCTAGAGAA	822
QY	279	MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgTyr	298
DB	823	ATGACACTGGCGGTTTGTAGATGTTGTTCATTATTCCCAATTTATGACACACGACGTAC	882
QY	299	ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr	318
DB	883	CCAAATGGAAACGAAAGACACAACTAACAGGGAAGTATATACAGATCCACTGGCGCGTA	942
QY	319	GlyValLeuGluSerGlyGlyArgThrTyrProTyrAsnProAsnAsnThrThrPhe	338
DB	943	AACGTGCTTCAATTGGTTCC-----TGGTATGAC---AAAGCACCTTCTTTC	987
QY	339	ThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrThrTrpLeuAsnArgIle	358
DB	988	GGAGTGATAGATCATCCGTTATTCGACCACCCCATGTTATTTGATTTATATACGGGACTC	1047
QY	359	PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly	376
DB	1048	ACAGTGATATACAAATCAAGAGCATTTCTTCGCTCGCTATATATAGACAT---TGGGCT	1104
QY	377	GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly	395
DB	1105	GGTCATCAAAATAGCTACCATCGTGTAGGGGTAGTAATCTTCACAAATATGATGGA	1164
QY	396	LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer	415
DB	1165	ACTATCAAAATCTACACAGCACTAGTACCTTTTGGATTTTACGAATATATGATTTACAAG	1224
QY	416	IleGluSer-----LeuAlaArgIleTyrLeuGlyThrGlyThrGluAlaAsn	430
DB	1225	ACTCTATCAAGGATGCGAGTACTCTTGATATTGTTTACCTGGTTATACG-----	1275
QY	431	AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle	449
DB	1276	---TATATATTT-----TTTGGAAATGCCAAGTCGAGTTTTTTCATGTGTAAACCAATTG	1326

Db 463 GAGTGGAGGAGNACCCCAACGGCTCCCGCGCCCTCCGCGAGCTGGCCAAACCGCTTCGAG 522
Qy 179 IleValAspAsnPhaPheGluIysAsnMetProLysPheLysGluAraGlnPheGluIle 198
Db 523 ATCTTCGAGCTCTTCAACCGATACATGCTCTCTCCGCGTGAACCACTTCGAGGTG 582
Qy 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuAspAla 218
Db 583 CCCTTCCTCACCCTGACCGCATGGCCCAACCTCCACTCTCTCTCAAGGACGCC 642
Qy 219 AspTyrPheGlyAlaGlnTyrGlnLeuGlyAspAspGluIleAraAspAsnTyrIleArg 238
Db 643 TCCATCTTCGGCGAGGTGGGCTGCTCCACCACCATCAACAACCTACTACGACCGC 702
Qy 239 LeuGlnGlyLeuIleArgGluTyrIysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 703 CAGATGAAGCTCACCGCCGAGTACTCCGACCACTCGCTGAAGTGTATGAGACCGGCTC 762
Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp 278
Db 763 GCCAAGCTCAAGGGCACCTCCGCCAAGCAGTGGGTGGACTACAACCATGTTCCGCGCGAG 822
Qy 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 823 ATGACCTTCGCGTCTCTGACGTGGTGGCCCTCTTCCCACTACGACACCCGCACTAC 882
Qy 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
Db 883 CCCATGGAGACCAAGGCCAGCTCACCCGCGAGGTGTACACGACCCGCTCGCGCGGTG 942
Qy 319 GlyValLeuGluSerGlyGlyArgThrTyrProTyrTyrAsnProAsnThrThrPhe 338
Db 943 AACGTGTCTCTCATCGGTCT-----TGGTACGAC---AAGGCCCCCAAGCTTC 987
Qy 339 ThrAlaMetGluAsnAlaAlaArgArgProSerTyrThrThrTyrLeuAsnArgIle 358
Db 988 GCGGTGATGAGTCTCTCGTATCGCGCGCGCGAGGTTCGACTACATACACCGGCTC 1047
Qy 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTyrGly 376
Db 1048 ACCGTGTACACCCAGTCCCGCTCCATCTCTCCGCGCGCTACATCCGCCAC---TGGGCC 1104
Qy 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
Db 1105 GGCCACCAAGATCTCTTACCACCGCGTGTCCCGCGGTCCCACTCCAGCAGATGTACGCG 1164
Qy 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
Db 1165 ACCAACCAAGACCTCCACTCCACCTCCACTTCGACTTCACCACTACGACATCTACAAG 1224
Qy 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
Db 1225 ACCCTCTCAAGGACGCGGTGCTCTCGACATCGGTGATCCCGCGGTACACCC----- 1275
Qy 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
Db 1276 ---TACATCTTC-----TTCGGCATCGCGAGGTGAGTCTTCTCATGTGTAACCAAGTCTC 1326
Qy 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
Db 1327 AACAAACACCGCAAGACCTCAAAATAC-----AACCCGCTGTCCAAGGACATC 1374
Qy 470 LeuSer-----GluLeuProGlyLysAspLysProArgProAsn 482
Db 1375 ATGGCTCCACCGCGGACTCCGAGCTCGAGTCTCCCGCGAGACTCCGACCGCCCAAC 1434
Qy 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer 502
Db 1435 TACGAGTCTTACTCCGACCGCTCTGCCACATCACTCCATCCCGCGCACCGGCAACACC 1494
Qy 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn 522
Db 1495 ACCGGCCTCGTGCG-----GTGTTCTCTCGACCCACCGCTCTGCAGACCTCAAC 1545

Qy 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyGlyAsn 542
Db 1546 AACACCATCTACTCCGACAAGATCACCCAGATCCCGCGTGAAGTCTGG---GACAAC 1602
Qy 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal 558
Db 1603 CTCCCTTCGTCCCGTGGTGAAGGGCCCCCGGCCACACCGCGCGGACCTCTCTCCAGTAC 1662
Qy 559 SerAspSerTyrHisSerLeuLysVal-----GlnAlaProGln 571
Db 1663 AACCGCTCCACCGGCTCCGTGGGCACTCTCTCCCGCGCTACGGCTTCGCCCTGGAG 1722
Qy 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 1723 AAGGCCGCGCAAGTACCGGTGCGCTCCGCTACGCCACT-----GACGCC 1767
Qy 592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
Db 1768 GACATCGTCTCCACGTGAACGACGCGCCAGATCCAG-----ATGCCCAAG 1812
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 1813 ACCATGAACCCCGCGGAGGACCTCACTCCAGACCTTCAAGTGGCGCGACGCCATCACC 1872
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 1873 ACCCTCAACCTCGCCACCGACTCTCTCCGCTCCAGCACAACCTCGCGGAGGACCCC 1932
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn 662
Db 1933 AACTCCACCTCTCCGGCATCGTGTACGTGGACCGCATCGAGTTTCATCCCGCTGGAC 1989

Search completed: January 20, 2006, 23:21:12
Job time : 1132 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 20, 2006, 22:34:18 ; Search time 7058 Seconds
(without alignments)
4520.939 Million cell updates/sec

Title: US-10-782-096-2

Perfect score: 3597

Sequence: 1 MNSYKNKYEMLDALRINS.....TFPNQSLKREQVNDLFIN 682

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cpn2.1/USPTO.spool/US10782096/runat.20012006.095215.24405/app.query.fasta_1.839
-DB=EST-QFMT=fastap -SUPFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10782096 @CGN 1.1.5315 @runat.20012006.095215.24405 -NCPU=6 -ICPU=3
-NO MWAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -DEV TIMEOUT=120 -WARN TIMEOUT=30
-THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hcc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121.5	3.4	2006	4	AY850327 Magnaporthe
2	117.5	3.3	11493	11	DQ051595 Homo sapi
3	117	3.3	782	10	CL651317 PRI0111d
4	113	3.1	2982	10	CL964901 OsIFCC011
5	110	3.1	1298	1	AJ537963 AJ537963
6	109.5	3.0	2823	10	CL967062 OsIFCC014
7	108	3.0	746	10	CL853210 OR_CBa008

8	108	3.0	2439	10	CL982610	CL982610 OsIFSC048
9	107.5	3.0	1437	10	CL967463	CL967463 OsIFCC039
10	107.5	3.0	1926	9	BH770523	BH770523 LLMGtag28
11	107	3.0	500	7	CO516871	CO516871 e13dSG98H
12	107	3.0	4979	4	BC032293	BC032293 Mus muscu
13	105	2.9	981	2	BI079460	BI079460 602873864
14	105	2.9	1016	3	BM904226	BM904226 AGENCOURT
15	105	2.9	3180	10	CL961241	CL961241 OsIFCC005
16	105	2.9	4379	4	BSM808965	BSM808965 Homo sapi
17	104.5	2.9	1193	8	DN729834	DN729834 CNB49-E02
18	104.5	2.9	2526	1	CL982730	CL982730 OsIFSC048
19	103	2.9	576	1	AW776556	AW776556 EST335621
20	103	2.9	676	2	BF647300	BF647300 NF018007E
21	103	2.9	592	3	BI308890	BI308890 EST530300
22	103	2.9	785	3	BQ165054	BQ165054 EST610923
23	102.5	2.8	1152	8	DN656547	DN656547 CEC23-G01
24	102.5	2.8	2646	10	CL980167	CL980167 OsIFCC034
25	102	2.8	2571	10	AY417032	AY417032 Mus muscu
26	102	2.8	72873	11	DQ051072	DQ051072 Homo sapi
27	101	2.8	702	5	BQ874517	BQ874517 QG15109.Y
28	100.5	2.8	830	10	CG459319	CG459319 FUIKJ967B
29	100.5	2.8	1434	10	CL965950	CL965950 OsIFCC013
30	100.5	2.8	3072	4	AK084557	AK084557 Mus muscu
31	100.5	2.8	3334	4	AK037516	AK037516 Mus muscu
32	100.5	2.8	3420	4	AK083596	AK083596 Mus muscu
33	100	2.8	607	2	BF651071	BF651071 NF100806E
34	100	2.8	645	6	CB215641	CB215641 NTSC.p008
35	100	2.8	1104	2	BG760743	BG760743 602717027
36	100	2.8	2094	4	CR626664	CR626664 full-leng
37	99.5	2.8	766	7	CO980294	CO980294 GM89007B1
38	99.5	2.8	1000	8	DR152948	DR152948 47519070
39	99.5	2.8	1128	8	DN702656	DN702656 CLJ42-H08
40	99.5	2.8	1266	8	DN702656	DN702656 CLJ42-H08
41	99.5	2.8	1626	10	AY419685	AY419685 Homo sapi
42	99.5	2.8	1740	10	CL946692	CL946692 OsIFSC000
43	99.5	2.8	2109	10	CL967870	CL967870 OsIFCC016
44	99	2.8	481	7	CO140775	CO140775 EST833446
45	99	2.8	518	7	CO144784	CO144784 EST819837

ALIGNMENTS

RESULT 1
AY850327
LOCUS Magnaporthe grisea cytochrome P450-like protein mRNA, complete cds.
DEFINITION
ACCESSION AY850327
VERSION AY850327.1 GI:58257422
KEYWORDS
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE
AUTHORS 1 (bases 1 to 2006)
TITLE Chen, B.S., Li, Y.Z., Peng, Y.L., Dong, H.T. and Li, D.B.
JOURNAL Submitted (08-DEC-2004) Guangxi University, Daxue Road 100, Nanning, Guangxi 530004, China
FEATURES
source
1..2006
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Y34"
/db_xref="taxon:148305"
/tissue_type="conidia; germ tubes; early appressoria; middle appressoria; late appressoria; mycelia"
49..1566
/codon_start=1
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VTEFGGEARREQFLKDAKPFYLEGFMKNVHKVTSPTDITTSVPASLESLKRLP


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RESULT 2
DQ051595
LOCUS      11493 bp      DNA      linear      GSS 02-JUN-2005
DEFINITION Homo sapiens TRRAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION  DQ051595
VERSION     DQ051595.1 GI:66904805
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 11493)
AUTHORS     Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
            Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
            White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE       A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
JOURNAL     (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED      15869325
REFERENCE   2 (bases 1 to 11493)
AUTHORS     Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
            Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
            White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE       Direct Submission
JOURNAL     Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment. Translation starts at the beginning of
            alignment.
FEATURES
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            /locus_tag="HC19616"
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Alignment Scores:
Pred. No.:      2.29      Length:      11493
Score:          117.50    Matches:     157
Percent Similarity: 34.4%  Conservative: 111
Best Local Similarity: 20.2% Mismatches:    314
Query Match:     3.3%     Indels:       197
DB:              11      Gaps:         38
US-10-782-096-2 (1-682) x DQ051595 (1-11493)
QY      2  AenSerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsn 21
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      8815 AACCTGGGAGGGAACACACCGCTGCACGACATGAGCGGTGTGAAGACCTGGAGGAAC 8874
QY      22  MetSerAsnCysTyrProArgTyrProLeuAlaLysAspProGln----- 36
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      8875 -----CGACTGCCCATCGTGTCTGACGACACTGTGCCCACTGGACGACG 8916
QY      37  ---MetThrMetArgAsnThrAsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThr 55
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      8917 ATCTTCATGTGGAGCGGACGATCATACACGGCGATTGTAACTGCCTATGAGATAGTCTCT 8976
QY      56  GlnPheIleGlyAspIleSerThrTyrSerSerProGluAlaAlaLeuSerValArgAsp 75
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      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      8977 CAG-----CATGATCCCGATTCAATAAGCGTATGCTTGGGGTTTCAT--- 9018
QY      76  AlaValLeuThrGlyIleAsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeu 95
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      9019 GCATCAGCTTCAGCGATCATCCAGTATGGAAATATCGCCCGGAAACAAGGA-----CTG 9072
QY      96  AlaSerGlnSerPheGlyIleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp 115
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db      9073 GTCAATGTGATCTCTGGATATATTAAGTCGGATCATACTATT----- 9114
QY      116  ProPheGluAlaLeuMetValLeuValGluGluLeuIleLysSerIleAspGlnArg 135
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      9115 -----CCAACTGTTCTCTATCGTGGATTGCTTCCAGAAG---ATTCCACAGCAA 9159
QY      136  ValArg-----GluAsnAlaLeuArgGluLeuGluGlyLeuGlnGlyIle 150
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      9160 GTTAAATGTACTCTCCAGCTGGCAGCGCTCATGGGCAAAAACGAGTGATCGCAGGCGCTT 9219
QY      151  MetArgLeuTyrGlnThrArgLeuGlnAlaTrpLeuValAsnLysAsnAspAspAsnArg 170
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db      9220 GAAGTTATTGAATCTACAAATTTAAATACTTC-----ACA 9255
QY      171  ArgAlaLeuValThrGlnTyrAlaIleValAspAsnPhePheGluLysAsnMetProLys 190
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      9256 AAAGAGATCACACCGCAATTTATGCACCTGAAGGGAATGTTCTTGCTCAGATCAACAAG 9315
QY      191  PheLysGluArgAsnPheGluIleLeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeu 210
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      9316 TCCGAGGAGGCAAAAC-----AAAGCCTTCTCTCAGCTGTGCAGATG 9357
QY      211  HisLeuIleLeuLeuArgAspAlaAspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAsp 230
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      9358 CACGATGTGCTGTGGTGA---GCCTGGGCCCATGTGGGGCGAC 9396
QY      231  GluIleArgAspAsnTyrIleArgLeuGlnGlyLeuIleArgGluTyrLysAspHis--- 249
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      9397 TACCTGGAGAAATCTTT-----GTGAAGGAGCGGCGAGCTGCACCTG 9438
QY      250  -----CysIleThrPheTyrAsnGlnGlyLeuAsnGlnPheAsnArgSerAsnAla 266
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db      9439 GCGTGTCTGCCATCACCTGCTACCTGCACGCGCTCGCGCATCAGAACGAGACAAATCG 9498
QY      267  GlnAspTrp-----ValSerPheAsnArgPheArgThrAspMet 279
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      9499 AGGAAATACTTAGCCCAAGGTGCTGTGGCTTTTGAGTTTTTGATGATGATCAACAACTTTG 9558
QY      280  ThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyrPro 299
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db      9559 GCAGATGCCGTGCACAGTACTGCTGTGTGGTGCCTA-----CCCATCCAGTGGCTG 9609
QY      300  LeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThrGly 319
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db      9610 GCCTGGATCCCACAGCTGCTCACCTGCTGTGGTGTGGCTCGAGGAGAAAGCTCTTGAAC 9669
QY      320  ValLeuGluSerGlyGlyArgThrTyrProTrp-----TyrAsnProAsnAsnThrThr 337
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db      9670 CTCATTAGCCAGGTTGGACGCGTATCCCAAGCGGTCTACTTTCCCATCCGAGACCTG 9729
QY      338  PheThrAlaMetGluAsnAsnAlaArgArgArg-----ProSerTyr 351
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db      9730 TACCTGACCTGAAATAGAACAGCGGGAACGCTACAGAGCGATCCAGGCGCCATAAGA 9789
QY      352  ThrThr-----Trp---LeuAsnArgIlePheValTyrThrArgThrLeu----- 365
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db      9790 GCACAGACCCCATGTGGCGCTGCAGCCGANTCATCATGCAGCGAGAGCTCCACCCC 9849
QY      366  -----GlyAsnMetSerAspValArgAsnIleTrp 375
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db      9850 ACCCTTCTGCTCTCCCTGGAGGCGATCGTGCATCATGTTCTGGTTTCAGAGAAAATTTGG 9909
QY      376  GlyGlyHisThrLeu-----ValGluAsnGly----- 384
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      9910 CATGAAGAGGTTCTCAGGCGAGCTCCAAACAGCGCGCTGGCGAAATGTTACTCCGTGGCGTTT 9969
QY      385  -----AsnAspGlySerGluIleThrHis-----AsnPhe---Gly 395
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db      9970 GAGAAAAGTGGAGCGGTGTCGATGCTAAATACCCCCCACACTCTCAATTTTGTGAG 10029
QY      396  LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPhe--- 414
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Db 10030 AAGTTGGTGGACGACGCTTTGGGGTGGCCCTGGAGATGTGTCCAAGCTCTCGACCATGTTTC 10089
QY 415 -----SerIleGluSerLeuAlaArgIleTyrLeuGlyGlyThrGluAlaAenAen 431
Db 10090 TCCAGCGCAGCTCTGAGTCTCTGGCCCG-----CGGGCG 10125
QY 432 TyrIleThrSerGlnTyrGlyValSerArgValIle-----PheAenThrSerAen 448
Db 10126 CAGGCCATCTGCACAGACCTCTTTCAGAGCTGAAGGCGCAGTTCACGACGGATTTT 10185
QY 449 IleAenAenValProGlySerLeuArgTyrGluValProAlaAenLeuProSer----- 466
Db 10186 GACTTCAGCGTTCAGGATCCATGAAGCTTCAT-----ATCTTATTTCTAAGTTG 10236
QY 467 GlnThrIleLeuSerGluLeuProGlyLysAenLysProArgProAenProAenAlaGlyAenPhe 486
Db 10237 AAAAAGTGGATCAAAATCTTGGAGGCCAAGACCAAGCAACTCCCAAAATCTTCTCTCAT 10296
QY 487 SerHisArgLeuSerTyrIleSerAenPheAenAlaArgSerSerSerGlyGlyIle 506
Db 10297 GAGGAAGAGTGGCGTCTTGTAGCAATTTCTCGGCACAGAC-AGCTGAAGTGGAAAT---- 10352
QY 507 ValSerLeuLeuThrPheGlyTyrAlaHisThrSerMetAspArgAenAenArgLeuGlu 526
Db 10353 -----TCCTGGGGAGTTCCTGTATGCCCAAGCCCAAGCCATTTATCAT 10394
QY 527 ProAspLysIleThrGlnIle-----AspAlaValLysGlyTyrPglyLysAenIle 543
Db 10395 CAAGATTGCACGCTTCATGCCCGGTAGAGATTGTGCAGAGACACACACCGCAGCCG 10454
QY 544 GlyPheValIleProGlyProThrGlyGlyAenLeuValLysValSerAspSerTyrHis 563
Db 10455 GCGGCTGTACATCCGGGG-----ACACAATGGCAA 10484
QY 564 SerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAla 583
Db 10485 GATCTACCCATACCTCGTCATGACGACGCGCTGCCTCAGAGTCACGCGGAGAGGCG 10544
QY 584 CysLeuValThrHisGlyAspAla-----IlePheValGluHisSerGlySerSerHis 601
Db 10545 TGTGTTGCAGCTGCTCGCTGCTGTAACCCCTGTTTGGAGAGAGAGAACACCAACAA 10604
QY 602 IleValSerPhePheAspCysSerAenSerSerGlyArg---ProSerAenThr-LeuLe 620
Db 10605 GAGGCACCTGTTTTTACAGTCCCCCGGGTGTGGCAGTTCCTCCCAAGATGCGCTCGT 10664
QY 620 uGluSerAspPheArgTyrIleAspValProGlyIlePheThrProSerIle----- 637
Db 10665 GGAGGACACCCCTCTTCACTTTCCTTGTGGAGATCTACAGACGCGTGCGCCAADA 10724
QY 638 -----AsnProLeuIleArgTyr-----ArgThrGlnSe 647
Db 10725 GGGCATCGAGCATGACACACCCATCTCCGCTTACTATGACCGCTGGCTACGCGTGCAG 10784
QY 647 PheGlyThrHisAlaIleAspLysPhe-----Gln 657
Db 10785 GCGGGGAACCAAGCCAGCCACCAAGTCTCTCCCGCATCTCCAGGAGGTTTCAGAGTAA 10844
QY 657 uPheIlePro-----LeuAenThrPheProAen 666
Db 10845 CATGTGTCGCGCAGCATGCTCAGAGAGTGGGCGCTGCACACCTTCCCCAAT 10896
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RESULT 3

CL651317/c
LOCUS
PRI011ld.D12 - PRI011ld.B21 (782) Mixed stage fosmid library of P.
DEFINITION
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.

ACCESSION
CL651317
VERSION
CL651317.1 GI:50129904
KEYWORDS
GSS.
SOURCE
Pristionchus pacificus

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ORGANISM  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 782)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geiseler,R. and Sommer,R.J.  
AppADB: an AcedB database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
JOURNAL  
PUBMED  
COMMENT  
14681447  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: raif.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
Location/Qualifiers  
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/db_xref="taxon:54126"  
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var. California"  
/note="Vector: pEpifos-5 Fosmid vector"  
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Alignment Scores:  
Pred. No.: 0.0316 Length: 782  
Score: 117.00 Matches: 68  
Percent Similarity: 36.8% Conservative: 37  
Best Local Similarity: 23.9% Mismatches: 104  
Query Match: 3.3% Indels: 76  
DB: 10 Gaps: 14  
US-10-782-096-2 (1-682) x CL651317 (1-782)  
QY 364 ThrLeuGlyAenMetSerAspValArgAenIleTyrPgly---GlyHisThrLeuValGlu 382  
Db 679 ACGTTGGCAATGCCGAGGCGTGTGTATATCGGTACGTATGATATACCTTGTCTGGAT 620  
QY 383 AenGlyAenAspGlySerGluIleThrHisAenPheGlyLys---ThrAspSerIleThr 401  
Db 619 AATGGCAACCATAGCTGGAGTCTGGCAGAGAAATCGCGCAAAATTACCCCTTCAACCACT 560  
QY 402 ProIleGlnTyrPheAenPheAlaAenLeuSerValPheSerIleGlu---SerLeuAla 420  
Db 559 GATGTGCTGATATATGGCGCCGCACACCGCTGGTATTTCATGCAGACTGGACACCGTG 500  
QY 421 ArgIleTyrLeuGlyGlyThrGluAlaAenAenTyrIleThrSerGlnTyrGlyValSer 440  
Db 499 CGTGAGCGCTCTGTAGCTAAAGCGCTTACTTACGTACGCGCATGCGGATTCGGCA 440  
QY 441 ArgValIlePheAenThrSerAenIleAenAenValProGlySerLeuArgTyrGluVal 460  
Db 439 -----ATTACACCCGCAACACGTGACCACTGATGCGGAGCTGCTTTTGAG--- 392  
QY 461 ProAlaAenLeuProSerGlnThrIleLeuSerGluLeuProGlyLysAenLysProArg 480  
Db 391 -----CAACATTCAGCGGCGCTGACCGCTCGGTATAGAT----- 359  
QY 481 ProAenAlaGlyAspPheSerHisArgLeuSerTyrIleSerAenPheAenAlaArgArg 500  
Db 358 -----AGCGCTTCTCCCGTGAAGAA 338  
QY 501 SerSerSerGlyGlyIleValSerLeuLeuThrPheGlyThrAlaHisThrSerMet--- 519  
Db 337 AGCAGTACA-----ATTCGCGGCTTGATCTTTGGTTACTCTCATTTCTGATATTGGT 287
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QY 520 ---AspArgAsnAnArgLeuGluProAspLysIleThrClnIleAspAlaValLysGly 538
Db 286 TTTGATCGCGCGCAAGGTAATATCGATAGCTATACC---CTGGGGGCTATGCGCGT 230
QY 539 TrpGlyGlyAsnIleGlyPheValIleProGlyProThrGlyGlyAsnLeuValLysVal 558
Db 229 TGGGAGCATCAGAACCGTGCCTATGTTGATGGG---GTGGTGAAGATT 185
QY 559 SerAspSerTrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTrpArgIle 578
Db 184 GAC----- 182
QY 579 ArgLeuArgTrpAlaCysLeuValThrHisGlyAspAlaIlePheValGluHisSerGly 598
Db 181 -----CGTTTGCACACACCATC-----CATGCAAG 155
QY 599 SerSerHisIleValSerPhePheAspCysSerAsnSerSerGlyArgProSerAnThr 618
Db 154 ATCAGTAAATGGGCAACAGGTTTGGCGATTACATAGTAACGCGCGGTGCTCAT--- 98
QY 619 LeuLeuGluSerAspPheArgTrpIleAspValProGlyIlePheThrProSerIleAsn 638
Db 97 ---GTTGAGAGCGGGTTCGTTGGGTTGACGATAGGGG-----ACTGTTAGA 53
QY 639 ProLeuIleArgTrp 643
Db 52 CCTATCTGGCCTTT 38
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RESULT 4
LOCUS CL964901
DEFINITION OeIFCC011268 Oryza sativa Express Library Oryza sativa (indica
cultiyar-group) genomic, genomic survey sequence.
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ACCESSION CL964901.1 GI:52384490
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VERSION Oryza sativa (indica cultivar-group)
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KEYWORDS Oryza sativa (indica cultivar-group)
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SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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ORGANISM Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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REFERENCE Ehrhartoidae; Oryzeae; Oryza.
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1 (bases 1 to 2982)
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AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
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Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
```

```
Wong, G.K.S., Deng, X.W. and Wang, J.
```

```
TITLE An analysis of transcriptional regulation of the rice genome and
```

```
its comparison to Arabidopsis
```

```
JOURNAL Unpublished (2004)
```

```
COMMENT Contact: Chen Chen
```

```
Department of Bioinformatic
```

```
Beijing Institute of Genomics
```

```
Chinese Academy of Sciences, Beijing 101300, China
```

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Tel: 86-10-80481559
```

```
Fax: 86-10-80488676
```

```
Email: chenchen@genomics.org.cn
```

```
Rice genomic sequence.
```

```
Class: exon-trapped.
```

```
FEATURES
```

```
Location/Qualifiers
```

```
source
```

```
1..2982
```

```
/organism="Oryza sativa (indica cultivar-group)"
```

```
/mol_type="genomic DNA"
```

```
/db_xref="taxon:39946"
```

```
/clone_lib="Oryza sativa Express Library"
```

```
/note="Oryza sativa exon trapped genomic sequences"
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```
ORIGIN
```

```
Alignment Scores:
```

```
Pred. No.: 0.839 Length: 2982
```

```
Score: 113.00 Matches: 137
```

```
Percent Similarity: 32.2% Conservative: 73
```

```
Best Local Similarity: 21.0% Mismatches: 204
```

```
Query Match: 3.1% Indels: 238
```

```
DB: 10 Gaps: 32
```

```
US-10-782-096-2 (1-682) x CL964901 (1-2982)
QY 43 AsnTrpLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 376 ACCCACTGAGCTACTCTCAACCTC-----AGCACCACTCTTTGGAAGTACATCCCA 429
QY 63 ThrTrpSerSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIleAsn 82
Db 430 TCTGAGCTCTCTCATGTTCCCGAGCTTAAATTTCTTGAC-----CTTAGCAACAACAT 483
QY 83 SerValGlyThrIleLeuSerAsnLeuGly---ValProLeuAlaSerGlnSerPheGly 101
Db 484 CTCCAAGGAGGACATCCCTTCTGTTTGGGAGCTTACCTTTGTACAAAACATAGTCCTT 543
QY 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAspPhe---GluAlaLeu 120
Db 544 GCCACAGCAGGCTTCAGGTGAAATA-----CCAGAGCTTTTAGGAACAGCAGATA 594
QY 121 MetValLeuValGluLeuIleLysSerIleAspGlnArgValArgGluAsnAla 140
Db 595 TCGCTCACATATGTTGACCTTGGAAACAACGGCTCTCACAGGGAGAATCCAGAGATCTCTG 654
QY 141 LeuArgGluLeuGlyLeuGlnGlyIleMetArgLeuTrpGlnThrArgLeuGlnAla 160
Db 655 GTAAATAGT---TCATCTCTACAA---GTGCTTAGGCTCATGAGAAATGCCCTTAGCGGA 708
QY 161 TrpLeuValAsnLysAsnAspAsnArgAlaLeuValThrGlnTrpAlaIleVal 180
Db 709 CAATCTCCCAACT---AATATGTTCAACTCGTCTCTCTT---ACTGACATTTGCCCTCCAA 762
QY 181 AspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeu 200
Db 763 CAGAACAGCTTTGGTGTACTATACCA----- 789
QY 201 LeuProValTrpAlaGlnAlaAlaAsnLeuLeuIleLeuLeuArgAspAlaAspTrp 220
Db 790 ---CCTGTTACTGCCATGCTTTCACAAAGTCAAGTAGTATCTTGATTTATCTGACAAACAATCTC 846
QY 221 PheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTrpIleArgLeuGln 240
Db 847 ATTGGAAACAATCGCTTCCTCAATAGGAAACCTTTCTTCGCTAATCTATGTTGCTCTTCA 906
QY 241 -----GlyLeuIleArgGluTrpLysAspHisCysIleThrPheTrpAsn 255
Db 907 CGAAACATTTTACTCGGAGCATTCCAGAGAGCTTAGGACATGCTCGCAACACTTGAGTT 966
QY 256 GlnGlyLeuAsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPhe 275
Db 967 ATATCCTTGAATAGCAACAATCTG----- 990
QY 276 ArgThrAspMetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTrpAspPro 295
Db 990 ----- 990
QY 296 ArgArgTrpProLeuAlaValLysThrGluLeuThrArgGluValTrpThrAspProVal 315
Db 990 ----- 990
QY 316 GlyPheThrGlyValLeuGluSerGlyGlyArgThrTrpTrpTrpTrpTrpTrpTrpTrp 335
Db 991 -----TCAGGGTCAGTACCCCAATCTCTCTTCAACATGCTCTCT 1029
QY 336 ThrThrPheThrAlaMetGluAsnAla-----ArgArgArgProSerTrpTrpThr 353
Db 1030 CTGACATTCCTTGGCCATGACAAATAACTCACTCATTTGGAAAAATTCCTTCAACATCGGC 1089
QY 354 TrpLeuAsnArgIlePheValTrpThrArgThrLeuGlyAsn-----Met 368
Db 1090 TAC-----ACTCTCCCAATATATTCAGGATTTGTTACTTG 1122
QY 369 SerAspValArgAsnIleTrpGlyHisThrLeuValGluAsnGlyAsnAspGlySer 388
Db -----
```

```
Db 1123 TCAGATGTC----- 1131
Qy 389 GluIleThrHisAsnPheGlyIysThrAspSerIleThrProIleGlnTyrPheAsnPhe 408
Db 1132 -----AAGTTTGATGTTGATCCCGACCTTCACTTCTCAATGCA 1170
Qy 409 AlaAsnLeuSerValPhe----- 414
Db 1171 TCAAATCTACAGACTTTTAACTGGCAAACTGGCTAACTGGGTCCATTCCACTGTTA 1230
Qy 415 ---SerIleGluSerLeuAlaArgIleTyrLeuGlyGlyThr-----GluAlaAsnAsn 431
Db 1231 GGGTCATTGCCAAATTTGAGAACTTGATTTAGGATTCAACATGTTTGAGGAGATGGA 1290
Qy 432 Tyr-----IleThrSerGlnTyrGlyValSerArgValIlePheAsnThr 446
Db 1291 TGGAGCTTTGCTCTCTCACTCACTAATGCTCTAGGTTGACTAGACTGATGCTGGATGG 1350
Qy 447 SerAsnIle----- 449
Db 1351 AACAAATNCCAAGGGAACCTGCCAAGTACTANTTGGAAATCTTCTAGTGATCTACAGTGG 1410
Qy 450 -----AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeu 464
Db 1411 TTGTGGCTAGGGCGCAACAACATTTCTGGTCTATACCAACAGAGATT---GCTAATCTC 1467
Qy 465 ProSerGlnThrIleLeu-----SerGluLeuProGlyIysAspIysProArg 480
Db 1468 AAGGCGCTCACTAAGTTGTACATGGATTACAATCTTTTGACTGGAAATATACCAACA 1527
Qy 481 -----ProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPhe 496
Db 1528 ATTGGAATTTACACACCTTGTCGATATATAAATTTACACAAAATTTATCTCAGAGTGG 1587
Qy 497 -----AspAla-----ArgArgSer 501
Db 1588 ATCCAGATGCTATTGGAATCTTTTGCAACTCTTAACCTGAGACTAGATAGGAACAAC 1647
Qy 502 SerSerGlyGlyLe-----ValSerLeuLeuThrPheGlyTyr 514
Db 1648 TTTAGTGAAGATATACCTGCAAGCATAGGCCAGTGCACCTCAACTTCAACACTCAACCTT 1707
Qy 515 AlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspIysIleThrGlnIle--- 533
Db 1708 GCTTAACTCAATTA-----AATGGAGCATACCGAGTAATCTTCAATTTAT 1758
Qy 534 -----AspAlaValIysGlyTyr-----GlyGlyAsnIleGlyPhe 545
Db 1759 CCTCTTCTGTTGTTTGGATTGTCACAAATTAATCTGCTGGAGGT----- 1806
Qy 546 ValIleProGlyProThrGlyGly-----AsnLeuValIysValSerAspSerTrpHis 563
Db 1807 ---ATTCCAGAGAGAAATGGCAACCTCGTTAATTTGAATATAAATCTCAGCATCTCAACAAT 1863
Qy 564 SerLeuIysValGlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAla 583
Db 1864 AGTTGCTGGTGAAGTTCATCC----- 1887
Qy 584 CysLeuValThrHisGlyAspAlaIlePheValGlu 595
Db 1888 -----ACTCTAGCGGAATGTGTGCTTCTAGAG 1914
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```
RESULT 5
AJ537963
LOCUS AJ537963 1298 bp mRNA linear EST 01-JUL-2004
DEFINITION AJ537963 1A1 Timarcha balearica cDNA clone Timarcha5F4, mRNA
sequence.
ACCESSION AJ537963
VERSION AJ537963.1 GI:40310965
KEYWORDS EST.
SOURCE Timarcha balearica
ORGANISM Timarcha balearica
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
```

```
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Chrysomeloidea; Chrysomelidae; Chrysomelinae; Timarchini; Timarcha.
1 (bases 1 to 1298)
Gomez-Zurita,J., Koplaku,F., Theodorides,K. and Vogler,A.P.
Resources for a phylogenomic approach in leaf beetle (Coleoptera)
systematics
(in) Jolivet,P., Santiago-Blay,J.A. and Schmitt,M. (Eds.); NEW
DEVELOPMENTS IN THE BIOLOGY OF CHRYSOMELIDAE, 19-35 (2004)
Contact: Gomez-Zurita J
Department of Entomology
The Natural History Museum
Cromwell Road, London SW7 5BD, United Kingdom.
FEATURES
Location/Qualifiers
1..1298
/organism="Timarcha balearica"
/mol_type="mRNA"
/db_xref="taxon:79517"
/clone="Timarcha5F4"
/dev_stage="adult"
/clone_lib="1A1"
/notes="country: Spain;Balearic Islands, Mallorca,
Esporles"
ORIGIN
Alignment Scores: 0.48 Length: 1298
Pred. No.: 110.00 Matches: 69
Percent Similarity: 39.2% Conservative: 52
Best Local Similarity: 22.3% Mismatches: 98
Query Match: 3.1% Indels: 90
DB: 1 Gaps: 19
US-10-782-096-2 (1-682) x AJ537963 (1-1298)
Qy 163 ValAsnLysAsnAspAsp-----AsnArgArgAlaLeu----- 173
Db 144 GTGAGCAAGAAATAAACAAGTTCAAAAGTCAATAACCGGATATCTTTTGAATCAATAAT 203
Qy 174 ValThrGlnTyrAlaIle-----ValAspAsnPhePheGluIysAsnMetPro 189
Db 204 ATCCAGAGATTACGATTATAATTTATAAAAAGTAGATAATTTCAAGCACCAACGTTGTC 263
Qy 190 LysPheLysGluArgAsnPheGluIleLeuLeuLeuProValTyrAlaGlnAlaAsn 209
Db 264 ACACACAGAAAGAAAAGTAAGGAATAC----- 290
Qy 210 LeuHisLeuIleLeuLeuArgAspAlaAspTyrPhe---GlyAlaGlnTrpGlnLeuGly 228
Db 291 -----GATTCGAAATATTTCTCGACGAGAAATGGAACACTACGAT 329
Qy 229 AspAspGluIleArgAspAsnTyrIleArgLeuGlnGlyLeuIleArgGlu---TyrLys 247
Db 330 CACGAAACATC-----TCAAAATCGAATTCGCCACTGTTTATCCACAAATTTCTATAAA 383
Qy 248 Asp-----HisCysIleThrPhe---TyrAsnGlnGly 257
Db 384 GATCAATCCGACACAAAACGTCCTCGATAGCACTTTGCGCTTTTATTCAACCAAT 443
Qy 258 LeuAsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThr 277
Db 444 AAAACAAATCGACGAGGATCATAGAT-----TTGAACCTTAACACGTTACAGCG 494
Qy 278 AspMetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArg 297
Db 495 GAAGAAACCAATTTGAGACCGCAATTTATATACTTTCTATTGGCCT----- 536
Qy 298 TyrProLeuAlaValIysThrGluLeuThrArgGluValTyrThrAspProValGlyPhe 317
Db 537 -----GTCCAAACACCTCGGCAATATATAAGAATCTGTA----- 572
Qy 318 ThrGlyValLeuGluSerGlyGlyArgThrTyrProTyrAsnProAsnThrThr 337
Db 573 -----GTGCTA-----AGGCTTTACCAAAATGAAAGACAAATCCACCGAGAT 614
```


Pred. No.: 0.331 Length: 746
Score: 108.00 Matches: 56
Percent Similarity: 36.2% Conservative: 28
Best Local Similarity: 24.1% Mismatches: 60
Query Match: 3.0% Indels: 88
DB: 10 Gaps: 11

US-10-782-096-2 (1-682) x CL853210 (1-746)

```
QY 171 ArgAlaLeuValThrGln-----TyrAlaIleValAspAsnPhePheGlu----- 185
DB 43 AAAGCCATTATCACCGATAAATCTTATCTGTCAGTTTAAATTTCTATGATTCANAG 102
QY 186 LysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeuLeuProValTyrAla 205
DB 103 TGAATATCCACTGATATATAAAAAAACATTT--GTCTATCTTTTGGCAGTA----- 153
QY 206 GlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAlaAspTyrPheGlyAlaGlnTrp 225
DB 154 -----AAATGTCATGTTATCTGCTCTAGCGTCGTGAACAACATGGGATCCATTCG 204
QY 226 GlnLeuGlyAspAspGluIleArgAspAsn-----TyrIleArgLeuGlnGlyLeu 242
DB 205 CAGATCTAGCGGACAGTACCATGACTACCCCGAGTAGCTGCCCAACTTACCGGCATA 264
QY 243 IleArgGluTyrIleAspHisCysIleThrPheTyr--AsnGlnGlyLeuAsnGlnPheA 262
DB 265 TGGCAAGAGGTAGAAATACATGTTATTGGTATCTGATTAATGCCGTCATGTCGAAGACT 324
QY 262 snArgSer-----TyrIleArgLeuGlnGlyLeu 267
DB 325 CAAGAGGTAGAGAAATACCTCATTTGTTAGTACCAGCAATGCAGCAGCTTTAGCGCG 384
QY 267 InAspTrpValSerPheAsnArgPheArgThrAspMetThrLeuThrValLeuAsp---- 285
DB 385 TCGATTTGTTCTTTCTTAAATTC-----TTAGATCCAT 420
QY 286 -----LeuAlaI 288
DB 421 CACTAGTGTGAAGTGGTGAAGGCTGAGATACATAAATTAGTAAGGCTCTTAGCTA 480
QY 288 IleLeuPheProAsnTyrAspPro---ArgArgTyrProLeuAlaValLysThrGluLeuT 307
DB 481 TATTGGGACACACCATACACTCTCTGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 539
QY 307 hrArgGluValTyrThrAspProValGlyPheThrGlyValLeuGluSerGlyGlyArgT 327
DB 539 ----- 539
QY 327 hrTyrProTyrAsnProAsnAsnThrThrPheThrAlaMetGluAsnAsnAlaArgA 347
DB 540 -----AGGAGTACTATTAAAGCTTACAATAATAATAAAGAA 576
QY 347 rgArgProSerTyrThrThrTrpLeuAsnArg 357
DB 577 AGAATCCACACTTT---GTATGGTCTACGAGG 605
```

RESULT 8

CL982610

LOCUS CL982610 2439 bp DNA linear GSS 21-BEP-2004
DEFINITION OsIFSC048386 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.

ACCESSION

CL982610

VERSION

CL982610.1 GI:52419702

KEYWORDS

GSS.

SOURCE

Oryza sativa (indica cultivar-group)

ORGANISM

Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzoideae; Oryza.

1 (bases 1 to 2439)

REFERENCE

AUTHORS

TITLE
JOURNAL
COMMENT

Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

FEATURES
source

1. 2439
Location/Qualifiers
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Alignment Scores:

Pred. No.: 2.32 Length: 2439
Score: 108.00 Matches: 145
Percent Similarity: 34.0% Conservative: 108
Best Local Similarity: 19.5% Mismatches: 255
Query Match: 3.0% Indels: 240
DB: 10 Gaps: 36

US-10-782-096-2 (1-682) x CL982610 (1-2439)

```
QY 3 SerTyrLysAsnLysAsnGlu-----TyrGluMetLeuAspAlaLeuArgIle 18
DB 436 AGTTACAGCATCGCGAGAAAACTTGACATGATCAATGGTAGGTTCCGAGGTTTC 495
QY 19 AsnSerAsnMetSerAsnCysTyrProArg-----TyrProLeuAlaLysAspPro 35
DB 496 AACCTTCGTCAGGATATATTTTCATCCGGGAAATATCTATACCATGACGAATCAGAGC 555
QY 36 GlnMetThrMetArgAsnThrAsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThr 55
DB 556 GATCCTATGTCACCAATACC-----TATCTGACCTATCAGAGGAAAAACAGT 603
QY 56 GlnPhe---IleGlyAspIleSer----- 62
DB 604 GAATTCACCATTTGGAACATCAATAAATTACTGGAACTTCTCTATTCCGAAAGGGCTC 663
QY 63 -----ThrTyrSerSerProGluAla----- 69
DB 664 GAATATGCCTACACTCTCCGGATAAAGACAAAAAATTGAAGCAGGTTTGTAGACCAG 723
QY 70 -----AlaLeuSerValArgAspAlaValLeuThr-----GlyIleAsnSerVal 84
DB 724 ACCTACAGCCTGATCGAAAGAAATTTCTTCTGAAATATGGTTATGGATTTTACACAGA 783
QY 85 GlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGlyIleIleSer 104
DB 784 GGAACC-----CTTGGGCTCAAAACGGTTCCTCGTAAT----- 816
QY 105 ArgLeuIleGlyIleLeuTrpAlaGlyProAspProPheGluAlaLeuMet-ValLeuVa 124
DB 817 ---ATCTCCGGAACCGTATATTTTTCAGGGATGATCTTACGAAAAAGCCACACATCATGTA 873
QY 124 lGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsnAlaLeuArg----- 142
DB 874 CGCGGAACAGATCTTCAGTATGCTTTCGGCAAAAGACTGGAGAACCAACCAAGGTGTAT 933
QY 143 -----GluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThr 156
DB 934 GCGGACTAGTTTCTACGAAATTAACAGCCTCGAAACCTTCCTCCCTCTTG- GAATC 992
QY 156 rArgLeuGlnAlaTrpLeu-----ValAsnLysAsnAspAsp----- 168
```

```
Db 993 ACAATATTCCGGAATGATCAAAAAGGTCAATCTGAACGGAAATATTATTTCTACAGCACAGA 1052
    :::: :::: :::: :::: ::::
Qy 169 -----AsnArgArgAlaLeuValThrGlnTyrAlaIleValAspAsnPh 184
    :::: :::: :::: :::: ::::
Db 1053 TTATTATCCCGGAAAACAGAAGAGGAATTTTG-----CAGATCCACAGAGATTTTC-- 1101
    :::: :::: :::: :::: ::::
Qy 184 eGluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeuLeuProValTy 204
    :::: :::: :::: :::: ::::
Db 1102 -----TCTACCATGATTTTCAAGACCATTAAT-----GTGTA 1133
    :::: :::: :::: :::: ::::
Qy 204 rAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAlaAspTyrPheGlyAla 224
    :::: :::: :::: :::: ::::
Db 1134 TGCCAAACATTACG-----GCTCCCATTTTTCCACCAA 1166
    :::: :::: :::: :::: ::::
Qy 224 nTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArgLeu----- 239
    :::: :::: :::: :::: ::::
Db 1167 GTTCTACTTTTACGACAACACCTGAATTTCAAGCAATCTAAGACTGGATACGGGAATCAA 1226
    :::: :::: :::: :::: ::::
Qy 240 -----GlnGlyLeuIleArgGluTyrLysAspHisCysI 251
    :::: :::: :::: :::: ::::
Db 1227 CTTCCCTAAAAGGAATTTCCGGATGGGACTTGGCTACCAAGTATCAGGAAGAAATTC 1286
    :::: :::: :::: :::: ::::
Qy 251 eThrPheTyrAsnGlnGlyLeuAsnGlnPheAsnArgSerAsnAlaGlnAsp----- 268
    :::: :::: :::: :::: ::::
Db 1287 CAATCTTATATAATATTTTCAATGCCCGCTTATGAGAACACGAAACAGCTGAAAGC 1346
    :::: :::: :::: :::: ::::
Qy 269 -----TrpValSerPheAsnArgPheArgThrAspMetTh 280
    :::: :::: :::: :::: ::::
Db 1347 ACAGCGTTTTACGGAAATACCTTTACCTGGCTGAGCTCTGATAAGCAACACTCCTCTATC-- 1404
    :::: :::: :::: :::: ::::
Qy 280 rLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyrProle 300
    :::: :::: :::: :::: ::::
Db 1405 -TTAAGCATGGACAGCGCTTGTTCAATATCCGACACAGATAAACAGCAGTTTCAGAC 1463
    :::: :::: :::: :::: ::::
Qy 300 uAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThrGlyVa 320
    :::: :::: :::: :::: ::::
Db 1464 GAAAGTA----- 1470
    :::: :::: :::: :::: ::::
Qy 320 lLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThr----- 336
    :::: :::: :::: :::: ::::
Db 1471 -----AGCGGAACCTACAGCTACAAATGGCTTACCGTGAACGGGATCTATCAGCAAG 1523
    :::: :::: :::: :::: ::::
Qy 337 -----ThrPheThrAlaMetGluAsnAsnAlaArg-----Ar 347
    :::: :::: :::: :::: ::::
Db 1524 AAGTTATTTCTTCCGAATATGCTTTTCAAAATGATGAACCAAGCACTCCCTACGA 1583
    :::: :::: :::: :::: ::::
Qy 347 GArgProSerTyrThrTrpLeuAsnArgIlePheValTyrThrArgThrLeuGlyAs 367
    :::: :::: :::: :::: ::::
Db 1584 AAAGCTTTCCCTTCGGCTTTGTCAATAAAAAATTTTC--TTCAACCGTCACTG--A-- 1635
    :::: :::: :::: :::: ::::
Qy 367 nMetSerAspValArgAsnIleTrpGlyHisThrLeuValGluAsnGlyAsnAsp 387
    :::: :::: :::: :::: ::::
Db 1636 -----AATGTCACCTTCAGG 1649
    :::: :::: :::: :::: ::::
Qy 387 ySerGluIleThrHisAsn-----PheGlyLysThrAspSer----- 399
    :::: :::: :::: :::: ::::
Db 1650 GOTTCTTATACGGATGATGTTCTGTACGGAATAATCGCCTTCCGGCTTTATGAACCTGAA 1709
    :::: :::: :::: :::: ::::
Qy 400 -IleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIleGluSerIle 419
    :::: :::: :::: :::: ::::
Db 1710 GTATTCAAGGGAATAATATGCTCTGTACCTGAACTCATCTTACTTTCAGT----- 1758
    :::: :::: :::: :::: ::::
Qy 419 uAlaArgIleTyrLeuGlyGlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyVa 439
    :::: :::: :::: :::: ::::
Db 1759 -----TATACTGCAGGAAGTTTTCACCAATAATCTGTTGACCGTGAAGCCGGTGT 1808
    :::: :::: :::: :::: ::::
Qy 439 lSerArgValIlePheAsnThrSerAsnIleAsnAsnValProGlySerLeuArgTyrGl 459
    :::: :::: :::: :::: ::::
Db 1809 AACCGTCAACCTTTAGAAACGACCCCTTGATCCGGGTAAAGAGGTGATATCAAAGCATTT 1868
    :::: :::: :::: :::: ::::
Qy 459 uValProAlaAsnLeuProSerGlnThrIleLeuSerGluLeuProGlyLysAspLysPr 479
    :::: :::: :::: :::: ::::
```

```
Db 1869 TGTCTATTATGACCTGAACGAAAAATAATATCTATGATGAG-----GGCGACAAA-- 1917
    :::: :::: :::: :::: ::::
Qy 479 oArgProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaAr 499
    :::: :::: :::: :::: ::::
Db 1918 -----GAAGCGGAGGCTATCTCTATTATGCTCAACAATATTTTCATTTAA 1961
    :::: :::: :::: :::: ::::
Qy 499 gArgSerSerGlyGlyIle-----Va 507
    :::: :::: :::: :::: ::::
Db 1962 AACCGACCCATCAGGTTCTATCAGTTACGTTCTCTATCCCTTATGGAAAGTATGCCCTGAA 2021
    :::: :::: :::: :::: ::::
Qy 507 lSerLeuLeuThrPheGlyTyrPheAlaHisThrSerMetAspArgAsnAsnArgLeuGluPr 527
    :::: :::: :::: :::: ::::
Db 2022 ACAGTCTATCCAGCAAGGCTGTTATAGCATGAACCGAA-----TTTACCCT 2069
    :::: :::: :::: :::: ::::
Qy 527 oAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyGlyAsnIleGlyPheValI 547
    :::: :::: :::: :::: ::::
Db 2070 AGACAAG-----CACCACTACTCTTTTGAGAT 2096
    :::: :::: :::: :::: ::::
Qy 547 ePro-----GlyProThrGlyGlyAsnLeuValLysValSerAspSerTrpHi 563
    :::: :::: :::: :::: ::::
Db 2097 CCTCTTTCATCAAAACGGAACGACCCAGGAAATAACTTACGACTTTGATTCCAAAAC 2156
    :::: :::: :::: :::: ::::
Qy 563 sSerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAl 583
    :::: :::: :::: :::: ::::
Db 2157 CGCAGTAG--ATTTTCACGCCCAAGTCGGAGTGTCTTATTTCAATATT--TACCGCAACGA 2213
    :::: :::: :::: :::: ::::
Qy 583 aCysLeuValThrHisGlyAspAlaIlePheValGluHisSerGlySerSerHisIleVa 603
    :::: :::: :::: :::: ::::
Db 2214 ACAGTTAGTACATCAT-----ATCATCACCAGTATGATACGGG-----GAATTTGC 2258
    :::: :::: :::: :::: ::::
Qy 603 lSerPhePheAspCysSer-----AsnSerSerGlyArgProSerAs 617
    :::: :::: :::: :::: ::::
Db 2259 CTCCTTCTCCCTCCGGAATTTACAGGATTGAACATAACAAAAACTCTCTGCCATCCA 2318
    :::: :::: :::: :::: ::::
Qy 617 nThrLeuLeuGlu 621
    :::: :::: :::: :::: ::::
Db 2319 TACCTATTTCGAA 2331
    :::: :::: :::: :::: ::::

RESULT 9
CL967463 1437 bp DNA linear GSS 21-SEP-2004
LOCUS OsIFCC039985 Oryza sativa Express Library Oryza sativa (indica
DEFINITION cultivar-group) genomic, genomic survey sequence.
ACCESSION CL967463
VERSION CL967463.1 GI:52389569
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 1437)
AUTHORS Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
Location/Qualifiers
source 1..1437
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
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/note="Oryza sativa exon trapped genomic sequences "

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ORIGIN
Alignment Scores:
Pred. No.:      1.11      Length:      1437
Score:          107.50    Matches:      78
Percent Similarity: 34.9%  Conservative: 55
Best Local Similarity: 20.5% Mismatches:    89
Query Match:      3.0%    Indels:      159
DB:              10      Gaps:       20

US-10-782-096-2 (1-682) x CU967463 (1-1437)
Qy 311 TyrThrAspProValGlyPhe-----ThrGlyValLeuGluSerGlyGlyArgThrTyr 328
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 112 TTCAAGGATGCATCGGCGAGCATCGGCGGGCGTCTGAGCTCTGGAAACAACACCACC 171
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 329 ProTrpTyrAsnProAsnAsnThr-----ThrPheThrAlaMet 341
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 172 CCTTTCTCGCGTGGAAATCGGGTGAATTCGGCCCGCGGAGCATCGGCTCACGGCGCTC 231
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 342 Glu-----AsnAsnAlaArgArgProSerTyrThrThrTyrLeuAsnArgIle 358
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 232 GAGCTCGCGGCCAGAACTTGACCGGTGCA----- 261
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 359 PheValTyrThrArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGlyGlyHis 378
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 262 --CTCGCGCGCGTCTCTCGGGAATCTGATTACTT-----CAC 300
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 379 ThrLeuValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyLysThrAsp 398
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 301 CTGCTTGACCTTCTCGTAAAT-----CGCTTCTCTGGCAGATACCTCGCCTGAAC 351
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 399 SerIleThrProIleGlnTyrPheAsnPheAlaAsn----- 410
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 352 AGTCTCGAAAAATTGCAAGTCCTCAACCTGAGTAACAATATTTGGACGGGATCAATTGCG 411
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 410 ----- 410
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 412 GACAGCGTTACAAACTGTTCCAGTTTGACGCGCTAGATTTCGAGCATAAACTTATTTCAA 471
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 411 -----LeuSerValPheSerIleGluSerLeuAlaArg 421
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 472 GGCCAGATTCCCTCGGCATAGGACTCTCTCTGAGCTGTCGATCTCGTCTCTCTCTCTG 531
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 422 IleTyrLeuGlyGlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGly----- 438
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 532 AATTATCTCTCGGG-----CACATTCTCTGAGCTCGGGAAGTTGTGCG 576
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 439 -----ValSerArgValIle 443
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 577 AATTTCGTCGTTGGACCTGAGTGTAAATATCATATCAGGTGAAATTCACGCGCCCTT 636
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 444 PheAsnThrSerAsnIle-----AsnAsnVal 452
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 637 TATAATCTCTCTCTCTCGGAATGCTATTCTTGGAGATGAATTCCTCGGGAAATCGTTG 696
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 453 ProGlySerLeuArgTyrGluValPro----- 461
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 697 CCGTCAAACATTGGCTATGCCCCTCTCTAATCTCCAATGGCTCTTATTGGGTGATAACATG 756
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 462 -----AlaLeuLeuProSerGlnThrIleLeuSerGluLeuProGlyLysAspLysPro 479
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 757 TTTCAAGGTATACATCCAGCA----- 777
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 480 ArgProAsnAlaGlyAspPheSerHis---ArgLeuSerTyrIleSer-----AsnPhe 496
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 778 -----TCCCTTGGCAACATTTTCACAGCTACATTTGATATATCTCTCAGAGAACGATTC 831
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 497 AspAlaArgSerSerSerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHis 516
   ::  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 832 TCTGGGCGAAATTCCTAGTCTCTCGGTAAAGCTTTCGAACCTGTCTGTCAACCTTCAGTAC 891
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QY 510 LeuThrPheGlyTrpAlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspLys 529
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Db 1737 TTAACCTTC-----AACATGATACCTTCGTGGGAAGA 1772
QY 530 IleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsnIleGlyPheValIleProGly 549
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Db 1773 ACCACA-----CCTAAC 1784
QY 550 ProThrGlyGlyAsnLeuValLysValSerAspSerTrpHis---Ser-LeuLysValG1 568
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Db 1785 TACTCATCTGGT-----GAGGCTAGCTCTCTCGCACGCTCTCCACTACCTTTGAG 1835
QY 568 nala---ProGlnArgGlnThrSerTyArgIle-----ArgLeuArgTyAlaCysIle 585
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Db 1836 GCATGCCACCAAGTGGCAACCACTACCACTCTTGACCGGACTGAGGCGCCAAATGCGCT 1895
QY 585 uValThrHisGly 589
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Db 1896 AGCTCCAGCAGGC 1908

RESULT 13
BI079460
LOCUS 602873864F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5005694 5',
DEFINITION mRNA sequence.
ACCESSION BI079460
VERSION BI079460.1 GI:14497790
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 981)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11045 row: p column: 15
High quality sequence stop: 764.
Location/Qualifiers
1..981
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/mol_type="mRNA"
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/clone="IMAGE:5005694"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
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/clone_lib="NCI CGAP Mam2"
/note="Organ: mammary; Vector: pCMV-SPT6; Site 1; SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN

Alignment Scores:
Pred. No.: 1.17 Length: 981
Score: 105.00 Matches: 93
Percent Similarity: 34.1% Conservative: 46
Best Local Similarity: 22.8% Mismatches: 125
Query Match: 2.9% Indels: 144
DB: 2 Gaps: 18
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US-10-782-096-2 (1-682) x BI079460 (1-981)
QY 283 ValLeuAspLeuAlaIleLeu---PheProAsnTyArgProArgArgTyTrpProLeuAla 301
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Db 4 GTCTGAACATCGGCGACCTCAGCTTTTCTGACGCGATCCT-----ACT 48
QY 302 ValLysThrGluLeuThrArgGluValTyThrAspProValGlyPheThrGlyValLeu 321
|||||
Db 49 GTACCACGCTTTTCCGGCGC-----GTGCTG 75
QY 322 GluSerGlyGlyArgTyTrpTrpTyArgProAsnAsnThrThrPheThrAlaMet 341
|||||
Db 76 GAGCGCGGATTCGCGCACTCCGATGAGCGCGGACACTCGGATC-----123
QY 342 GluAsnAsnAlaArgArgProSerTyThrThrTrpLeuAsnArgIlePheValTy 361
|||||
Db 124 -----AATGCACAAAGAAGACGGTCTCAAGCGCCATACTCTAACAGGCGGTTAGCCAA 177
QY 362 ThrArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGlyGlyHisThrLeuVal 381
|||||
Db 178 ACAAAGACAAGTGCTAGGAAGCAA-----201
QY 382 GluAsnGlyAsnAspGlySerGluIleThr-HisAsnPheGlyLysThrAspSerIleTh 401
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Db 202 -----TCCCATGGAGTAGGCTAAGTGTCCACCTACTTCCATGAGTGACTTTCATAGA 252
QY 401 rProIleGlnTyPheAsnPheAlaAsnLeuSer-----412
|||||
Db 253 ACCCTAAAGTCTATTTTTGTGAGGCTACCTTTGAGGGGCTCTCAAGCCAAAAGAGAG 312
QY 413 -----ValPheSerIleGluSerLeuAlaArgIleTyrlue 424
|||||
Db 313 ACTAGTGGCGTTGTACCCATAGTCAGTTGGCAGATCGACTGCTTCAAGGTCGTGGGC 372
QY 424 u---GlyGlyThrGlu-----AlaAsnAsnTyrlleThrSerGlnTyArgLys 439
|||||
Db 373 GCCTGGAGGACAGACACCCCGGACTCTGCTAAGGAATATCTTACTAAGTCCCGCAGAT 432
QY 439 l-SerArgVal-----IlePheAsnT 446
|||||
Db 433 COTCCACTGTGATGCCAGACCCAGTGTGAAGCCAGCACCAAGTACCAGAAGTGGCCGCT 492
QY 446 hrSerAsnIleAsnAsnValProGlySerLeuArgTyTrpGluValProAlaAsnLeuProS 466
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Db 493 CCTCAGACGGGAGAGCAGTGGGGAAGCCTGGAGCTACACCTTCTGACTGGAGGCCCC 552
QY 466 erGlnThrIleLeuSerGluLeu-----ProGlyLysAspLysProArgProAsnAlaG 484
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Db 553 CCTCAACCTCGCTCCGGGTCTAACAGCCCTTGGCAAAAGGAAGCAGAAACTGAGATTAT 612
QY 484 lAspPheSerHisArgLeuSerTy-----IleSerAsnPheAspAlaArgArgS 501
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Db 613 CAGTATTTTCAGCAGGAAGTGGACCAAGGGGTTCCTCTCTCCCAA---GAGCCACGCTAGGA 669
QY 501 erSerSerGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspA 521
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Db 670 GTAGGAGTGTGATGTCTCATCCTTTGGCTAGC-----701
QY 521 rgAsnAsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyG 541
Db 702 -----TCCT 705
QY 541 lAsnIleGlyPheValIleProGly-----ProThrGlyGlyAsnLeuValLysV 558
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Db 706 TCAATCTTACCTTTTGTCTACCTGTGAGCCAGGCGCAGACAGACAGTGGAGAACCTGGTGC 765
QY 558 alSerAspSerTrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyArgI 578
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QY 578 leArgLeuArgTyTrpAlaCysLeuValThrHisGlyAspAlaIlePheValGluHisSerG 598
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Db 786 -----GGCAGCTTTGTCGAATGGCTGGTCTCTTTTGGCAGGATCCTG 831

Qy 598 lySerSerHisIleValSerPheAspCysSerAenSerSerGly-----A 614

Db 832 GAAAGAAACAGATCCTT-----AAGGCTTCTGGTCTTCCAGGTGACA 873

Qy 614 qpProSerAenThrLeuGluSerAspPheArgTyrIleAspVal-----P 630

Db 874 GGCACGAACACCTTGGTGGCTCTCTGGCGATGAATGTGGTTGGGAACACAC 933

Qy 630 roGlyIlePheThrProSer 636

Db 934 GAGGCTTTCTCACACCATCC 953

RESULT 14

LOCUS BM904226 1016 bp mRNA linear EST 12-MAR-2002

DEFINITION AGENCOURT 6693004 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5499692

5', mRNA sequence.

ACCESSION BM904226

VERSION BM904226.1 GI:19354603

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 1016)

NIH-MGC <http://mgi.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Lou Staudt

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLML2133 row: g column: 21

High quality sequence stop: 659.

FEATURES

source

1. 1016

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5499692"

/tissue_type="lymphoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 85"

/note="Organ: lymph; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.23 Length: 1016

Score: 105.00 Matches: 61

Percent Similarity: 34.5% Conservative: 38

Best Local Similarity: 21.3% Mismatches: 86

Query Match: 2.9% Indels: 102

DB: 3 Gaps: 13

US-10-782-096-2 (1-682) x BM904226 (1-1016)

Qy 304 ThrGluLeuThrArgGlu-----ValTyrThrAspProValGlyPheThr 318

Db 70 ACAGATATATCCATACCTACGTCAGCGTGCCTCTCTGCAATCACAGGCAGTTCGCGGACG 129

Qy 319 GlyValLeu-----GluSerGlyGlyArgThrTyr 328

Db 130 CTTCTCTCTCCACAATTTCTGCACATGCTGTCTCTCCCGCTCTTCTGGCATCCACAGCCGAG 189

Qy 329 ProTyrPheAsnProAenThrThrPheThrAlaMetGluAenAenAlaAsgArgArg 348

Db 190 CCTTTCATCCCGGAGCAGCGCTCTGTCACGCACGACGACGCGCCCTCTCTGAACCGG 249

Qy 349 ProSer---TyrThrThrTrpLeuAenArgIlePheValTyrThrArgThrLeuGlyAen 367

Db 250 CGGTCTGCTTCTCAGTACA-----GTCCAGAGCAGCAGCTGCGCGCAC 291

Qy 368 -----MetSerAspValArgAenIleTrpGlyGly----- 377

Db 292 ACGTCCGCAACCTCAGTCTGGGTCTACCCGCGCTCTTTGGAGGGGCTCTGTCTTAGC 351

Qy 378 -----HisThrLeuValGluAenGlyAenAspGlySerGluIleThr--- 391

Db 352 CACCCTTCTAGGTATCACCGAGAAATAGTCTCTGGGTTCACAGGATCTGAGTGGACCCGG 411

Qy 392 -----HisAenPheGlyLysThrAspSerIleThrProIleGlnTyrPhe 406

Db 412 ACAGTACTCAGTCTGAATCTCCGCTCTGAGCGGGAATCCATGCCCGCCGACAG----- 465

Qy 407 AsnPheAlaAsnLeuSerValPheSerIleGluSerLeuAlaArgIleTyrLeuGlyGly 426

Db 466 -----ACCAGTGCCTCTTCTGGTGTGCTGTCTGTCTGAGCAGCAGGAGGAGTGGC 519

Qy 427 ThrGluAlaAsnThrIleThrSerGlnTyrGlyValSerArgValIlePheAenThr 446

Db 520 TCTCAGGATCTGTGTACACTTCAGCCACAGAGGG----- 555

Qy 447 SerAenIleAenAsnValProGlySerLeuArgTyrGluValProAlaAenLeuProSer 466

Db 556 -----AGGGGTTTTCGCGCA 570

Qy 467 GlnThrIleLeuSerGluLeuPro---GlyLysAspLysProArgProAenAlaGlyAsp 485

Db 571 TCAGGGTTGGCACTCAGTCAAGTGGAGGGAATGGCTCCAGCCGCAAACTCGGCGCAGC 630

Qy 486 PheSerHisArgLeuSerTyrIleSerAenPheAspAlaArgSerSerSerGlyGly 505

Db 631 ATTGCGCATGACCTT-----CAGTGTGACCTGAGAGCTTCTTT----- 669

Qy 506 IleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAenAenArgLeu 525

Db 670 -----CTG 672

Qy 526 GluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyAenIleGlyPhe 545

Db 673 GAGTATGACCGGCTTCAAGAGCTGGATCAGAGCCTTTGAGTGGGAGAGCTCC----- 723

Qy 546 ValIleProGlyProThrGly 552

Db 724 -----CCAGACCCCAACAGGG 738

RESULT 15

LOCUS CL961241

DEFINITION OsIECC005799 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION CL961241

VERSION CL961241.1 GI:52377209

KEYWORDS GSS.

SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 3180)

Ma,L., Wang,C., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.

An analysis of transcriptional regulation of the rice genome and

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 20, 2006, 22:58:38 ; Search time 326 Seconds
(without alignments)
3718.703 Million cell updates/sec

Title: US-10-782-096-2

Perfect score: 3597

Sequence: 1 MNSYKRNKYEMLDALRINS.....TFPNOSLEKRBQVNDLFIN 682

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFMT=fastcap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCUI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_WMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -DEV TIMEOUT=120 -WARN TIMEOUT=30
-THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
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2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCITUS COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	942.5	26.2	3507	2	US-08-315-468-3 Sequence 3, Appli
2	940.5	26.1	3504	3	US-10-089-678-2 Sequence 2, Appli
3	940.5	26.1	3690	3	US-10-089-678-3 Sequence 3, Appli
4	910.5	25.3	4173	3	US-09-661-322A-37 Sequence 37, Appl
5	901.5	25.1	3471	2	US-07-876-280-29 Sequence 29, Appl
6	901.5	25.1	3471	2	US-07-812-180A-1 Sequence 1, Appli
7	901.5	25.1	3471	2	US-08-315-468-1 Sequence 1, Appli
8	901.5	25.1	3471	3	US-07-941-650A-1 Sequence 7, Appli
9	897	24.9	3684	2	US-08-448-170-7

10	897	24.9	3684	3	US-08-961-803-5	Sequence 5, Appli
11	894	24.9	3684	3	US-09-661-322A-62	Sequence 62, Appl
12	892	24.8	8854	3	US-09-053-549-1	Sequence 1, Appli
13	889	24.7	3558	3	US-09-178-252-22	Sequence 22, Appl
14	889	24.7	3558	3	US-09-826-660-22	Sequence 22, Appl
15	886.5	24.6	4074	2	US-08-377-690-1	Sequence 1, Appli
16	880	24.5	3624	2	US-07-951-715A-6	Sequence 6, Appli
17	880	24.5	3624	2	US-08-459-448A-6	Sequence 6, Appli
18	880	24.5	3624	3	US-08-459-595A-6	Sequence 6, Appli
19	880	24.5	3624	3	US-08-459-504B-6	Sequence 6, Appli
20	880	24.5	3624	3	US-08-459-444-6	Sequence 6, Appli
21	880	24.5	3624	3	US-09-053-549-7	Sequence 7, Appli
22	880	24.5	3624	3	US-09-547-422-6	Sequence 6, Appli
23	880	24.5	3624	3	US-09-988-462-6	Sequence 6, Appli
24	872	24.2	1929	3	US-09-178-252-24	Sequence 24, Appl
25	872	24.2	1929	3	US-09-826-660-24	Sequence 24, Appl
26	868.5	24.1	2133	3	US-09-661-322A-41	Sequence 41, Appl
27	855	23.8	1953	2	US-08-315-468-5	Sequence 5, Appli
28	855	23.8	1953	3	US-07-941-650A-3	Sequence 3, Appli
29	849.5	23.6	2159	3	US-08-286-870A-7	Sequence 7, Appli
30	843	23.4	3934	2	US-08-100-709-3	Sequence 3, Appli
31	843	23.4	3934	2	US-08-176-865-3	Sequence 3, Appli
32	843	23.4	3934	2	US-08-474-038-3	Sequence 3, Appli
33	843	23.4	3934	2	US-08-779-046-3	Sequence 3, Appli
34	843	23.4	3934	2	US-08-881-340-3	Sequence 3, Appli
35	842.5	23.4	1959	3	US-09-661-322A-5	Sequence 5, Appli
36	841.5	23.4	2430	6	PCT-US92-00040-1	Sequence 1, Appli
37	840.5	23.4	1956	3	US-08-996-441B-51	Sequence 51, Appl
38	840.5	23.4	1956	3	US-08-993-722A-51	Sequence 51, Appl
39	840.5	23.4	1956	3	US-08-993-170A-51	Sequence 51, Appl
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41	840.5	23.4	1956	3	US-09-427-770-51	Sequence 51, Appl
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43	840.5	23.4	2965	2	US-08-460-570-1	Sequence 1, Appli
44	840.5	23.4	2965	2	US-08-460-570-2	Sequence 2, Appli
45	840.5	23.4	2965	3	US-08-286-870A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-315-468-3
; Sequence 3, Application US/08315468
; Patent No. 5554534
; GENERAL INFORMATION:
; APPLICANT: Michaels, Tracy Ellis
; APPLICANT: Poncerrada, Luis
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Process for Controlling Scarab Pests
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,468
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,941
; FILING DATE: 01 FEB 1993
; APPLICATION NUMBER: 07/828,430
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/808,316
 FILING DATE: 16-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MAY73.C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3507 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Bacillus thuringiensis
 STRAIN: kumamotoensis
 INDIVIDUAL ISOLATE: 50C
 IMMEDIATE SOURCE:
 LIBRARY: LambdaGEM-11(tm) library of L. Poncerrada
 CLONE: 50C(b)
 US-08-315-468-3

Alignment Scores:
 Pred. No.: 3,528-90 Length: 3507
 Score: 942.50 Matches: 249
 Percent Similarity: 50.3% Conservative: 115
 Best Local Similarity: 34.4% Mismatches: 272
 Query Match: 26.2% Indels: 87
 Ds: 2 Gaps: 27

US-10-782-096-2 (1-682) x US-08-315-468-3 (1-3507)

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199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuileLeuLeuArgAspAla 218
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703 CAATGAAACTTACTGCGAGATATTTCTCACCACCTGTGTAAAGTGTATGAACTGGTTA 762
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397 ThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerile 416
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417 GluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsnAsn 431
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Qy 654 AspIysPheGluPheIleProLeuAsn---ThrPhe---ProAsnGlnSerLeuIys 671
Db 1972 GATAAGTTGCAACTTATTCGGTAAATGCAACATTTGAAGCAGAGAAGACCTAGATGTG 2031
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RESULT 3

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US-10-089-678-3
; Sequence 3, Application US/10089678
; Patent No. 6962977
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: SHININ HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AND METHOD
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
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; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-089-678-3
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Alignment Scores:

Pred. No.:	6,26e-90	Length:	3690
Score:	940.50	Matches:	256
Percent Similarity:	51.8%	Conservative:	111
Best Local Similarity:	36.1%	Mismatches:	288
Query Match:	26.1%	Indels:	56
DB:	3	Gaps:	23

US-10-782-096-2 (1-682) x US-10-089-678-3 (1-3690)

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Qy 43 AsnTyrIysGluTrpLeuAsnMetCysAsp---SerAsnThrGlnPheIleGlyAspIle 61
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Qy 62 SerThrTyrSerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 367 GAGACGTTTATTAGT-----TCATCTACGGTTCAAACTGGAATTT 405
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 406 GGCATTGTGTGTCAGTACTGGGGGCTTTAGGGGTTCCATTTGCTGGACAGATAGCTAGT 465
Qy 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyPro-----AspProPheGluAla 119
Db 466 TTTTATAGTTTCATGTGCTGGTCAATTATGGCCATCAAGTACCGTGAGTGTATGGGAATG 525
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Qy 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
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Db 112 -----TCTTTGTGTATAGCGGGAATAATATCAATCCCACTGTTGTCGCATCAACA 165
Qy 67 ProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyLeuAsnSerValGlyThr 86
Db 166 -----GTCCAAACGGGTATTAAACATAGCTGGTAGA 195
Qy 87 IleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGlyIleIleSerArgLeu 106
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Qy 107 IleGlyIleLeuTrp---AlaGlyProAspProPheGluAlaLeuMetValLeuValGlu 125
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Qy 166 AsnAspAsnArgArgAla---LeuValThrGlnTyrAlaIleValAspAsnPhePhe 184
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Db 556 GCTCAAGCTGCAAAATTACACTATTATTATTGAGNAGTCTCTCTTTTGGTAGTAA 615
Qy 225 TrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArgLeuGlnGlyLeuIleArg 244
Db 616 TTTGGCTTACATCGCAGGAAATTCACCGTTATTATGAGCGCAAGTGGCAACAAACGAGA 675
Qy 245 GluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeuAsnGlnPheAsnArgSer 264
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Qy 365 LeuGlyAsnMetSerAspValArgAsnIle-----TrpGlyGlyHisThrLeuValGlu 382
Db 1024 TCATCAGATGAGTGCTACTAGGCATATGACTTACTGCGGGGGGACACAATTCATCT 1083
Qy 383 AsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyLysThrAsp---SerIleThr 401

Db 1084 CGGCCAATAGGAGCGGATTAAATACCTCAACGCTGGGTCTACCAATCTTCTTAAAT 1143
Qy 402 ProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIleGluSerLeuAlaArg 421
Db 1144 CTTGTAAAGA---TTATCAATCTTCTCGAGACGTATATGAGCTGAATCATATCAGGA 1200
Qy 422 IleTyrLeuGlyGlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSerArg 441
Db 1201 GTGCTTCTATGGGGAATTT-----TACCTTGAACCTATTTCATGGTGGTCCCTACT 1248
Qy 442 ValIlePheAsnThrSerAsnIleAsnAsnVal-----ProGlySerLeuArgTyrGlu 459
Db 1249 GTTAGATTAAATTTTAGGAACCTCAGAACTACTTTTGAAGAGGTACTGCTAACTATAGT 1308
Qy 460 ValProAlaAsnLeuProSerGlnThrIleLeu-----SerGluLeuProGlyLys 476
Db 1309 CAACCTATAGTACCTGGGCTCAATTAAAGAGATTCAGAACTGAATATACCAAGAA 1368
Qy 477 AspLysProArgProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPhe 496
Db 1369 ACAACAGAACGACCAATATGATCATATAGTATAGTATCTCATAGGCGCTCAT 1428
Qy 497 AspAlaArgArgSerSerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHis 516
Db 1429 TCACAATCTAGG-----GTGCAATGTACCAGTATATTTCTTGGACGCAC 1470
Qy 517 ThrSerMetAspArgAsnAsnArgLeuGluProAspLysIleThrGlnIleAspAlaVal 536
Db 1471 CGTAGTCAGATCGTACAAATACCAATAGTTCAGATAGCATAAACAATATCCATTGGTA 1530
Qy 537 LysGlyTyrGlyGlyAsnIleGlyPheValIle-----ProGlyProThrGlyGly 553
Db 1531 AAATCAATTCACCTTAATTCAGTACCTCTGTAGTCAGTGGCCAGGATTACAGAGGG 1590
Qy 554 AsnLeuValLysValSerAspSerTrpHisSerLeuLysValGlnAlaProGlnArgGln 573
Db 1591 GATATAATCCGAACCTAACGTTAATGGTAGTGTACTAAGTATGGGTCTTAAATTTAATAAT 1650
Qy 574 ThrSer-----TyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAsp 590
Db 1651 ACATCAATTCAGCGGTATCGGTGAGATTTCGTTATGCTGCTTCTCAACAATG----- 1704
Qy 591 AlaIlePheValGluHisSerGlySerHisIleValSerPhePheAspCysSerAsn 610
Db 1705 GTCTCGAGGTAACTGTCGGAGGAGTACTACTTTTGTATCAAGGATTCCTAGTACTATG 1764
Qy 611 SerSerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValPro 630
Db 1765 AGTGCA-----AATGAGTCTTTGACATCTCAATCATTTAGATTTGCAAAATTCCT 1815
Qy 631 -----GlyIlePheThrProSerIleAsnProLeuIleArgTyrArg 644
Db 1816 GTAGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATAGTAATATGACAGT 1875
Qy 645 ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn---Thr 663
Db 1876 AGACAAACGTT-----CATTTCATAAAATTTGAATTCATTCCAATTAATCAAC 1926
Qy 664 PheProAsnGln---SerLeuGluLysArgGluGlnIleValAsnAspLeuPheIleAsn 682
Db 1927 TTGGAAGCAGAAATACGATTTAGAAGGGCGCAAGGGGGTGAATGCTCTGTTTAAAT 1986
RESULT 5
US-07-876-280-29
; Sequence 29, Application US/07876280
; Patent No. 5262158
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Begley, Angela L.
; TITLE OF INVENTION: NO. 5262158el Bacillus thuringiensis Isolates for
; TITLE OF INVENTION: Controlling Acarides
; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/876,280
 ; FILING DATE: 19920430
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saliwanchik, David R.
 ; REGISTRATION NUMBER: 31,794
 ; REFERENCE/DOCKET NUMBER: M/S 104
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 904-375-8100
 ; TELEFAX: 904-372-5800
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3471 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Bacillus thuringiensis
 ; STRAIN: kumamotoensis
 ; INDIVIDUAL ISOLATE: PS50C
 ; IMMEDIATE SOURCE:
 ; CLONE: E. coli NM522 (pMYC2320) NRRL B-18769
 ; US-07-876-280-29

Alignment Scores:
 Pred. No.: 8,576-86 Length: 3471
 Score: 901.50 Matches: 249
 Percent Similarity: 49.3% Conservative: 113
 Best Local Similarity: 33.9% Mismatches: 267
 Query Match: 25.1% Indels: 105
 DB: 2 Gaps: 26

US-10-782-096-2 (1-682) x US-07-876-280-29 (1-3471)

QY 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
 DB 4 ACTCCAAATCAATCAAAATGAATATGAATATAGATCGCACACCT---TCTACATCTGTA 60
 QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
 DB 61 TCCAGTGATTCTAACAGATACCTTTTGGCAATGAGCCCAACAGATCGGTTACAAAATATG 120
 QY 43 AsnTyrLysGluTrpLeuAsnMetCys---AspSerAsnThrGlnPheIleGlyAspIle 61
 DB 121 AATTATAAGAGATTATCTGAAATGTCTGGGGAGAGAAATCTCGAATATTATTGGAATCCG 180
 QY 62 SerThrTyrSerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
 DB 181 GAGACGTTTATTAGT-----TCAATCCAGATTCAAACTGGAAAT 219
 QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
 DB 220 GGCATTGTTGGTTCGAATACTAGGAGCTTTAGGGTTCCATTGCTAGTCAGATAGTAGT 279
 QY 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyPro-----AspProPheGluAla 119
 DB 280 TTCTATAGTTTCATTGTTGGTCAATTATGCGCGTCAAAGAGCGGTAGATATATGGGGAGAA 339

QY 120 LeuMetValLeuValGluGluLeuIleLysSerIleAspGlnArgValArgGluAsn 139
 DB 340 ATTATGGAACGAGTGGAAAGAACTCGTTGATCAAAAATAGAAAAATATGTAAAGATAAG 399
 QY 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
 DB 400 GCTCTTGTCTGAATTAAGAGGCTAGGAATGCTTTGGATGTATATCAGCAGTCACGTGA 459
 QY 160 AlaTrpLeuValAsnLysAsnAspAsnArgAlaLeuValThr---GlnTyrAla 178
 DB 460 GATTGGCTGGAANAATCGCAATGATGCAAGAACTAGAGAGTGTGTTCTAATCAATTATA 519
 QY 179 IleValAspAsnPheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
 DB 520 GCTTTAGATCTTAACCTTTGTTAGTTCAATTCATCTTTTCAGTATCCGACACGAAGTA 579
 QY 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuIleLeuLeuLeuArgAspAla 218
 DB 580 CTATTATTAGCAGTATATGCACAGGCTGTGAACCTACATTTATTGTTATTAAAGATGCT 639
 QY 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
 DB 640 TCTATTTTGGAGAGAGTGGGGATTACACAGGTGAATTTCTAGATTTTATATATCGT 699
 QY 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
 DB 700 CAAGTCAACTTACCGCTGAATATTCAAGACTATTGTTAAAGTGTATAAATCGCGCTTA 759
 QY 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
 DB 760 GATAAATTGAAAGGTACCACTTCTAAAGTTGGCTGAATTTATCATCATGTTCCGTAGAG 819
 QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
 DB 820 ATGACATTACTGTTAGATTGTTGGCGGTTATTTCCAAACTATATGACACACATATGTAT 879
 QY 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
 DB 880 CCAATCGAAACAACAGCTCACTTACACGGGATGTGTATACAGATCCGATAGCATTT--- 936
 QY 319 GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338
 DB 937 AACATAGTGCACAGTACTGGATTCTGCAACCCCTGGTCAACCCACAGTGGTATCTTTT 996
 QY 339 ThrAlaMetGluAsnAsnAlaArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
 DB 997 TATGAAGTTGAAACAACAGTAATTCGTCGCCACACTGTTGATATATCTCAGCTCAGTA 1056
 QY 359 PheValTyrThrArg-----ThrLeuGlyAsnMetSerAspValArgAsnIle 374
 DB 1057 GAAATTAATACAGTAGAGGGGTATTAGTTTAAATAATATGATGCATATATA---AATAC 1113
 QY 375 TrpGlyGlyHisThrLeuValGluAsnGlyAsnAspGlySerGluIleThrHis----- 392
 DB 1114 TGGTCAGGACATACCCCTAAATATCGTAGACAGCTGATTCGACCGCTAAACATACACAG 1173
 QY 393 AsnPheGlyLysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSer 412
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 QY 413 ValPheSerIleGluSerLeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn----- 430
 DB 1204 TCATTTGCACCTTAGGATAGGATATTTTGAATAATTAATTCACCTGTGGCAACCTAGCT 1263
 QY 431 AsnTyrIleThrSerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnIleAsn 450
 DB 1264 AATTACTACCAAAAGCATATGCT----- 1287
 QY 451 AsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIleLeu 470
 DB 1289 ---GTGCCGGGATCTTGGTTCCATATGTTGGTAAAGGGGAACCTCATCAACACAGCGTAT 1344

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QY 471 -----8er 471
Db 1345 TTATATTCAAAACACATACAGCTCTCCAAGGGGTACACAGTTTATGAATCAAGTGAT 1404
QY 472 GluLeuProGlyLysAspLysProArgProAlaAlaGlyAspPheSerHisArgLeuSer 491
Db 1405 GAAATACCT--CTAGATAGAACTGTACCGGTAGCTGAAAGCTATAGTCATAGATTATCT 1461
QY 492 TyrIleSerAsnPheAspAlaArgSerSerGlyGlyIleValSerLeuLeuThr 511
Db 1462 CATATTACCTCCCACTCTTCTCAAAAATGGGAGTGCACTATGGGAGTTTCCCTGTA 1521
QY 512 PheGlyTyrAlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspLysIleThr 531
Db 1522 TTTGTTGGACACATAGTACGCGATTTAAATATATACATATATTCAGATAAATCACT 1581
QY 532 GlnIleAspAlaValLysGly-----TrpGlyGlyAsnIleGlyPheValIle 547
Db 1582 CAATTCACGCGGTAAGGACATGTTATATCTAGGGGGTTCC-----GTAGTA 1632
QY 548 ProGlyPro-----ThrGlyGlyAsnLeuValLysValSerAsp-----Ser 561
Db 1633 CAGGGTCTCGGATTTACAGGAGGAGATATATTAAGAACCAATCTAGCATATATAGGG 1692
QY 562 TrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArg 581
Db 1693 ACCTTTGGGTTACAGTAATAGGTGCTTATCACAA---AGATATCGTGTAAAGATTCG 1749
QY 582 TyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHisSerGlySerHis 601
Db 1750 TATGCTCTTACAACA-----GATTTGAATTTACTATACCTTGGCGACACAATA 1800
QY 602 IleValSerPhePheAspCysSerAsnSerSerGlyArgProSerAsnThrLeuLeuGlu 621
Db 1801 GAAAAAATAGATTTTAAACAAAATCTAGTAATAGGGCA-----TCITTAAGTAT 1851
QY 622 SerAspPheArgTyrIleAspValProGlyIlePheThrProSerIleAsnProLeuIle 641
Db 1852 GAAACATTTTAA-----TTGCGAAGTTTCAATGACTGATTTCCAA 1890
QY 642 ArgTyrArgThrGln-----SerPheGlyThrHisAla-----652
Db 1891 TTCAGAGAAACACAGATAAAATACCTCTATCCATGGGTGATTTAGTCCGGTCAAGAA 1950
QY 653 -----IleAspLysPheGluPheIleProLeuAsn---ThrPhe---ProAsnGlnSer 668
Db 1951 GTTTATATAGACCGAATCGAATTCATCCAGTAGATGACACATATGAGCGGGAACAAGAT 2010
QY 669 LeuGluLysArgGluGlnValAsnAspLeuPheIleAsn 682
Db 2011 TTAGAAGCGGCGAAGAACGATGATGCTTGTGTTACGAAT 2052

RESULT 6
US-07-812-180A-1
; Sequence 1, Application US/07812180A
; Patent No. 5366892
; GENERAL INFORMATION:
; APPLICANT: Foncerrada, Luis R
; APPLICANT: Payne, Jewel M
; APPLICANT: Sick, August J
; TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus
; TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding a
; TITLE OF INVENTION: Coleopteran-Active toxin
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Roman Saliwanchik
; STREET: 2421 N.W. 41st Street, Ste A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/812.180A
; FILING DATE: 19920102
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDAEM (TM) - 11 LIBRARY OF LUIS
; CLONE: 50C
; LIBRARY: FONCERRADA
US-07-812-180A-1

Alignment Scores:
Pred. No.: 8,578-86 Length: 3471
Score: 901.50 Matches: 249
Percent Similarity: 49.3% Conservative: 113
Best Local Similarity: 33.9% Mismatches: 267
Query Match: 25.1% Indels: 105
DB: 2 Gaps: 26

US-10-782-096-2 (1-682) x US-07-812-180A-1 (1-3471)
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QY 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 4 AGTCCAAATATCAAAATGAATATCAAAATATAGATGCGACACCT--TCTACATCTGTA 60
QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 61 TCCAGTGATTTCTTAACAGATACCCCTTTTGGATGAGCCAAACAGATGCGTTACAAAATATG 120
QY 43 AsnTyrLysGluTyrLeuAsnMetCys---AspSerAsnThrGlnPheIleGlyAspIle 61
Db 121 AATTATAAGATTATCTGAAAATGCTGGGGGAGAGATCTCGAATATTATTTGGAAATCCG 180
QY 62 SerThrTyrSerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 181 GAGACGTTTATTAGT-----TCAATCCACGATTCACAACTGGAAT 219
QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 220 GGCATTGTTGGTGAATACTAGGAGCTTTAGGGGTTCCATTTGCTAGTCAGATAGCTAGT 279
QY 102 IleIleSerArgLeuIleGlyIleLeuTyrAlaGlyPro-----AspProPheGluAla 119
Db 280 TTTTATAGTTTCATTTGGTCAATATTATGGCGCTCAAGAGCGTAGATATATGGGAGAA 339
QY 120 LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
Db 340 ATTATGGAAACGAGTGGAGAACTCTTGTATCAAAAATAGAAAATATATGTAAAGATAAG 399
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QY 160 AlaTyrLeuValAsnIysAsnAspAspAsnArgArgAlaLeuValThr---GlnTyrAla 178
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QY 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
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QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 820 ATGACATTATCGTATTAGATTGGTGGCGTTATTTCCAACTATGACACACATATGTAT 879
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QY 319 GlyValLeuGluSerGlyArgThrTyrProTyrAsnProAsnAsnThrThrPhe 338
Db 937 AACATAGTGACAGTACTGATTCGCAACCTTGGTCAACCCACAGTGGTATCTTTT 996
QY 339 ThrAlaMetGluAsnAsnAlaArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
Db 997 TATGAAGTTGAAACAAACGTAATTCGTCGCCACACTTGTGTATATATCTACGTCAGTA 1056
QY 359 PheValTyrThrArg-----ThrLeuGlyAsnMetSerAspValArgAsnIle 374
Db 1057 GAAATTAATACAGTAGAGGGGTATTACGTTAAATAATGATGCATATATA---AACTAC 1113
QY 375 TrpGlyGlyHisThrLeuValGluAsnGlyAsnAspGlySerGlyLeuThrHis----- 392
Db 1114 TGGTCAGACATACCTTAAATATCGTAGAACAGCTGATTCACCGTACATACACAGCT 1173
QY 393 AsnPheGlyLysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSer 412
Db 1174 AATTACGGTCCGAATCACTTCA-----GAAAAAGAT 1203
QY 413 ValPheSerIleGluSerLeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn----- 430
Db 1204 TCATTGCACTTGAGGATAGGATATTTTGAATTAATTCACCTGTGGCAACCTAGCT 1263
QY 431 AsnTyrIleThrSerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnIleAsn 450
Db 1264 AATTACTACAAAGCATATGCT----- 1287
QY 451 AsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIleLeu 470
Db 1288 ---GTGCGGGATCTTGGTTCATATGTTAAAAAGGGGAACCTCATCAACACAGGTAT 1344
QY 471 -----86r 471
Db 1345 TTATATTTCAAAACACATACAGCTCTCCAAGGTGTACACAGGTTTATGAATCAAGTGTAT 1404
QY 472 GluLeuProGlyLysAspLysProArgProAsnAlaGlyAspPheSerHisArgLeuSer 491
Db 1405 GAAATACCT---CTAGATAGAACTGTACCGGTAGCTGAAGCTATAGTATAGTATATCT 1461
QY 492 TyrIleSerAsnPheAspAlaArgSerSerSerGlyIleValSerLeuLeuThr 511

RESULT 7

US-08-315-468-1
; Sequence 1, Application US/08315468
; Patent No. 5554534

GENERAL INFORMATION:

; APPLICANT: Michaels, Tracy Ellis
; APPLICANT: Poncerrada, Luis
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Process for Controlling Scarab Pests
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,468
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,941
; FILING DATE: 01 FEB 1993

/ APPLICATION NUMBER: 07/828,430
/ FILING DATE: 30-JAN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/808,316
/ FILING DATE: 16-DEC-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: MAY3.C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3471 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Bacillus thuringiensis
/ STRAIN: kumamotoensis
/ INDIVIDUAL ISOLATE: PS50C
/ IMMEDIATE SOURCE:
/ LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF LUIS
/ LIBRARY: FONCERRADA
/ CLONE: 50C(a)
/ US-08-315-468-1

Alignment Scores:
Pred. No.: 3471
Score: 8,57e-86 Length: 3471
901.50 Matches: 249
Percent Similarity: 49.3% Conservative: 113
Best Local Similarity: 33.9% Mismatches: 267
Query Match: 25.1% Indels: 105
DB: 2 Gaps: 26

US-10-782-096-2 (1-682) x US-08-315-468-1 (1-3471)

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QY 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
DB 4 AGTCCAAATAATCAAAATGAATATGAATATAGATGCGACACCT---TCTACATCTGTA 60
QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
DB 61 TCCAGTGAATCTTAACAGATACCCCTTTTGGGAATGAGCCCAACAGATGCGTTACAAAATATG 120
QY 43 AsnTyrLysGluTyrLeuAsnMetCys---AspSerAsnThrGlnPheIleGlyAspIle 61
DB 121 AATTATAAGATTATCTGAAATGCTGGGGGAGAGAAATCCTGGAATATTTCGAAATCCG 180
QY 62 SerThrTyrSerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
DB 181 GAGACGTTTATTAGT-----TCAATCCACGATTCAAACTGGAATT 219
QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
DB 220 GGCATTGTTGGTCGAATACTAGGAGCTTTAGGGTTCCATTGCTAGTCAGATAGCTAGT 279
QY 102 IleIleSerArgLeuIleGlyIleLeuTyrAlaGlyPro-----AspProPheGluAla 119
DB 280 TTCTATAGTTTCATTGCTGCTCAATTTATGCGCGTCAAGAGCGTAGATATATGCGGAGAA 339
QY 120 LeuMetValLeuValGluLeuIleLysSerIleAspGlnArgValArgGluAsn 139
DB 340 ATTATGGAACGAGTGGAGAACTCGTTGATCAAAAAATAGAAAAATATGTTAAAGATAAG 399
QY 140 AlaLeuArgGluGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
DB 400 GCTCTTGCTGAATTAAGAGGCTAGGAAATGCTTTGGATGTATATCAGCAGTCACTTGAA 459
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QY 160 AlaTyrLeuValAsnLysAsnAspAspAsnArgAlaLeuValThr---GlnTyrAla 178
DB 460 GATTGGCTGGAAATCGCAATGATCCAAGAACTAGAGTGTGTTCTTAATCAATTATA 519
QY 179 IleValAspAsnPheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
DB 520 GCTTTAGATCTTAACCTTTGTTAGTTCAATTCCTTTTGCAGTATCCGACACGAAGTA 579
QY 199 LeuLeuLeuProValTyrAlaGlnAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
DB 580 CTATTATTAGCAGTATATGCACAGCTGTGAACCTACATTTATTGTTATTAGAGATGCT 639
QY 219 AspTyrPheGlyAlaGlnTyrGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
DB 640 TCTATTTTGGAGAGAGTGGGATTTACACCGGTGAAATTTCTAGATTTTATATCGT 699
QY 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
DB 700 CAAGTGCAACTTACCGCTGAATATTTCAGACTATTGTGTAAGTGGTATAAAATCGGCTTA 759
QY 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp 278
DB 760 GATAAATTTGAAAGGTACCACCTTCTAAAGTTGGCTGAATTTATCATCAGTTCGATGAGAG 819
QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgTyr 298
DB 820 ATGACATTTACTGTTATGATTTGTTGGCTGTTATTTCCAACTATGACACACATATGTTAT 879
QY 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
DB 880 CCAATCGAAACCAACAGCTCAACTTACCGGATGTGTATACAGATCCGATGCAATTT--- 936
QY 319 GlyValLeuGluSerGlyGlyArgThrTyrProTyrTyrAsnProAsnAsnThrThrPhe 338
DB 937 AACATAGTACAGACTGCTGGATTTGCAACCCCTTGGTCAACCCACGACGTTGTTCTTTT 996
QY 339 ThrAlaMetGluAsnAlaArgArgProSerTyrThrThrTyrLeuAsnArgIle 358
DB 997 TATGAAGTTGAAACACAGTAATTCGTCGCCACACTGTTTGTATATCTAGCTCAGTA 1056
QY 359 PheValTyrThrArg-----ThrLeuGlyAsnMetSerAspValArgAsnIle 374
DB 1057 GAAATTAATATACAGTAGAGGGGTATTACGTTAAATAATATGATCATATATA---AACTAC 1113
QY 375 TrpGlyGlyHisThrLeuValGluAsnGlyAsnAspGlySerGluIleThrHis----- 392
DB 1114 TGGTCAGACACATACCCTAAATATATCGTAGAACAGCTGATTCGACCGTAACATACACAGCT 1173
QY 393 AsnPheGlyLysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSer 412
DB 1174 AATTACGTCGTAATCACTTCA-----GAAAAAGAAAT 1203
QY 413 ValPheSerIleGluSerLeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn----- 430
DB 1204 TCATTTGCACCTTGGAGATAGGATATTTTGAATAATTAATTCACCTGTGGCAAACTAGCT 1263
QY 431 AsnTyrIleThrSerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnIleAsn 450
DB 1264 AATTACTACAAAAGCGATATGTT----- 1287
QY 451 AsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIleLeu 470
DB 1288 ---GTGCGGATCTTGGTTCCATATGTTAAAGGGGAACTCATCAACACAGCGTAT 1344
QY 471 -----Ser 471
DB 1345 TTATATTCAAAAACACATACAGCTCTCTCAAGGGGTGTACACAGGTTTATGAATCAAGTAT 1404
QY 472 GluLeuProGlyLysAspLysProArgProAsnAlaGlyAspPheSerHisArgLeuSer 491
DB 1405 GAAATACCT---CTAGATAGCACTGTACCGGTAGCTGAAGAGCTATAGTATGATATCT 1461
QY 492 TyrIleSerAsnPheAspAlaArgArgSerSerSerGlyGlyIleValSerLeuLeuThr 511
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1462 CATATTACCTCCATTTCTTCTCTAAATAATGGAGTGCATACATATGGAGTTCCTCGTGA 1521
512 PheGlyTyrAlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspLysIleThr 531
1522 TTGTTTGGACATACATAGTCGGATTTAAATATACATATATTCAGATAAATCAT 1581
532 GlnIleAspAlaValLysGly-----TrpGlyGlyAsnIleGlyPheValIle 547
1582 CAAATTCACGCGTAAAGCGAGACATGTTATATCTAGGGGTTCC-----GTAGTA 1632
548 ProGlyPro-----ThrGlyGlyAsnLeuValLysValSerAsp-----Ser 561
1633 CAGGGTCCTGGATTTACAGAGAGAGATATATTAAGAAACCAATCCTAGCATATPAGG 1692
562 TrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArg 581
1693 ACCTTTGCGGTACAGTAATGGTGTATATCAAA--AGATATGCTGTAGATTCGC 1749
582 TyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHisSerGlySerHis 601
1750 TATGCTCTACAA-----GATTTTGAATTTACTCTATACCTTGGCGACACAATA 1800
602 IleValSerPhePheAspCysSerAsnSerSerGlyArgProSerAsnThrLeuLeuGlu 621
1801 GAAATAAATAGATTTTAAACAAACTATGGATATGGGGCA-----TCCTTAACGTAT 1851
622 SerAspPheArgTyrIleAspValProGlyIlePheThrProSerIleAsnProLeuIle 641
1852 GAAACATTTAA-----TTGCGAAGTTTCAATTAAGTATTCGAA 1890
642 ArgTyrArgThrGln-----SerPheGlyThrHisAla-----652
1891 TTCAGAGAAACACAAGATAAAATACCTCATCCATGGGTGATTTAGTCCGCTCAAGAA 1950
653 -----IleAspLysPheGluPheIleProLeuAsn---ThrPhe---ProAsnGlnSer 668
1951 GTTTATATAGACGAATCGAATTCATCCAGTAGATGAGACATATGAGCGGGAACAGAT 2010
669 LeuGluLysArgGluGlnGluValAsnAspLeuPheIleAsn 682
2011 TTAGAAGCGCGAAGAAACAGTGAATGCTTGTGTACGAAT 2052

RESULT 8
US-07-941-650A-1
; Sequence 1, Application US/07941650A
; Patent No. 6294184
; GENERAL INFORMATION:
; APPLICANT: Uyeda, Kendrick A.
; APPLICANT: Bradfisch, Gregory A.
; TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/941,650A
; FILING DATE: 19920908
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/758,020
; FILING DATE: 12-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/658,935
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; FILING DATE: 21-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,112
; FILING DATE: 16-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; CLONE: E. coli NM522 (pmYC1638), NRRL B-18751
; US-07-941-650A-1
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Alignment Scores:
Pred. No.: 8 57e-86 Length: 3471
Score: 901.50 Matches: 249
Percent Similarity: 49.3% Conservativeness: 113
Best Local Similarity: 33.9% Mismatches: 267
Query Match: 25.1% Indels: 105
DB: 3 Gaps: 26
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US-10-782-096-2 (1-682) x US-07-941-650A-1 (1-3471)

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QY 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
DB 4 AGTCCAAATAATCAAAAATGAATATGAATATATAGATGCGACACCT---TCTACATCTGTA 60
QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAnthr 42
DB 61 TCCAGTGAATCTAACAGATACCCCTTTTGGCAATGAGCCACAGATCGTTACAAAATATG 120
QY 43 AsnTyrLysGluTyrLeuAsnMetCys---AspSerAsnThrGlnPheIleGlyAspIle 61
DB 121 AATTATTAAGATTATCTGAAATGCTGGGGAGAGAAATCTCGAATATTATTGGAAATCCG 180
QY 62 SerThrTyrSerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
DB 181 GAGACGTTTATTAGT-----TCATCCACGATTCAAACTGGAATT 219
QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
DB 220 GCGATTGTTGGTCGAATACTAGGAGCTTTAGGGGTTCCATTTGCTAGTCAGATAGTAGT 279
QY 102 IleIleSerArgLeuIleGlyIleLeuTyrAlaGlyPro-----AspProPheGluAla 119
DB 280 TTCTATAGTTTCATTGTTGTCATATATGCGCGTCAAGAGCGTAGATATATGGGAGAA 339
QY 120 LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
DB 340 ATTATGGAACGAGTGGNAGAACTCGTTGATCAAAAAATAGAAAAATATGTAAAGATAAG 399
QY 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
DB 400 GCTCTTGTGAAATTAAGGGCTAGGAAATGCTTTGGATGTATATCAGCAGTCACCTTGA 459
QY 160 AlaTyrLeuValAsnLysAsnAspAspAsnArgAlaLeuValThr---GlnTyrAla 178
DB 460 GATTGCTGGAATAATCGCAATGATGCAAGAACTAGAAAGTGTGTTTCTAATCAATTTATA 519
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;
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Salivanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-448-170-7

Alignment Scores:
Pred. No.:          2,86e-85           Length:          3684
Score:              897.00             Matches:           252
Percent Similarity: 50.7%             Conservative:      104
Best Local Similarity: 35.9%           Mismatches:       274
Query Match:        24.9%             Indels:            72
DB:                  2                 Gaps:              24

US-10-782-096-2 (1-682) x US-08-448-170-7 (1-3684)

QY   7 LysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerPheAsnMetSerAsnCysTyr 26
     |||||
Db   16 AAAAAATGCAATGAAATTATAAATCTTTATCGATTCAGCT---GTATCGAATCATTC 72

QY   27 ProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThrAsnTyrLysGlu 46
     ::::
Db   73 GCACAAATGAATCTATCAACCGATCTCGTATT-----GAGGAT 111

QY   47 TrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSerThrTyrSerSer 66
     ||||
Db   112 AGCTTGTTGTAATGCCGAGGGGAC-----NATATCGATCCATTGTGTAGC 156

QY   67 ProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIleAsnSerValGlyThr 86
     ||||
Db   157 -----GCATCAACAGTCCAAACGGGTATTAACATAGTAGCTGTAGA 195

QY   87 IleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGlyIleIleSerArgLeu 106
     ||||
Db   196 ATACTAGGTGTATTAAGCGGTACCGTTCTCGACAAAATAGTAGTTTTTATAGCTTTCT 255

QY   107 IleGlyIleLeuTrp---AlaGlyProAspProPheGluAlaLeuMetValLeuValGlu 125
     ::::
Db   256 GTTGFGAATTATAGCCCCGGCGGAGAGATCCTTGGGAAATTTCCTAGAACATGTCBAA 315

QY   126 GluLeuIleLysGlySerIleAspGlnArgValArgGluAsnAlaLeuArgGluLeuGlu 145
     ::::
Db   316 CAACATTATAAGACAACAAGTAACAGAAAATACTAGSGATACGGCTCTTGCTCGATTACAA 375

QY   146 GlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGlnAlaTrpLeuValAsnLys 165
     ::::
Db   376 GGTTTAGGAAATTCCTTTTAGAGCCCTATCAACAGTCACCTTGAAGATTGGCTAGAAAAACCGT 435

QY   166 AsnAspAspAsnArgArgAla---LeuValThrGlnTyrAlaIleValAspAsnPhePhe 184
     ::::
Db   436 GATGATGCAAGAACGGAAGGTGTTCTTTATACCCAATATATAGCTTAGAACCTTGATTT 495

QY   185 GluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeuLeuProValTyr 204
     ::::
Db   496 CTTAATGCCATGCCGCTTTCCGAATTAGAAACCAAGAGTTCCTATTATATGGTATAT 555

QY   205 AlaGlnAlaAsnLeuHisLeuIleLeuLeuArgAspAlaAspTyrPheGlyAlaGln 224
     ::::
Db   556 GCTCAAGCTGCAAAATTACACTATATATTATGAGAGATGCCTCTCTTTTGGTAGTGA 615
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Db 676 GAATATTCTGATTATTGCGCAAGATGGTATATATACCGGTTTAAATAATTGAGAGGACA 735
Qy 265 AenAlaGlnAspTyrValSerPheAenArgPheArgThrAspMetThrLeuThrValLeu 284
Db 736 AATGCTGAAGTGGTGGATATATCAATTCGCTAGAGACTTAAGCGCTAGAGTATTA 795
Qy 285 AspLeuAlaIlePhePheProAenTyrAspProAenArgTyrProLeuAlaValIleThr 304
Db 796 GATCTAGTGGCACTATTCCCAAGCTATGACACGCGTGTATTCCAATGAATACCAAGTGT 855
Qy 305 GluLeuThrArgGluValTyrThrAspProValGlyPheThrGlyValLeuGluSerGly 324
Db 856 CAATTAACAGAGAAATTTATACATCCATTTGGAGACAAATGCA---CCTTCAGA 912
Qy 325 GlyArgThrTyrProTyrThrAsnProAenThrThrPheThrAlaMetGluAenAsn 344
Db 913 TTTGCAAGTACCAATTTGGTTTAAATAATATGACCATCGTTTCTGCCATAGAGCTGCC 972
Qy 345 AlaArgArgArgProSerTyrThrThrTrpLeuAenArgIlePheValTyrThrArgThr 364
Db 973 GTTATTAGGCTCCGCATCTACTTGTATTTCCAGAACACAGCTTACAAATTTTCAGC---GTA 1029
Qy 365 LeuGlyAenMetSerAspValArg-----AenIleTrpGlyGlyHisThrLeuValGlu 382
Db 1030 TTAAGTCGATGGAGTAATACTCAATATATGAATTACTGGTGGGACATAGACTTGAATCG 1089
Qy 383 AenGlyAenAspGlySerGluIleThrHisAenPheGlyLysThrAsp---SerIleThr 401
Db 1090 CGAACAAATAGGGGGTCATTAGTACTCGACACAGCGGAATACCAATCTCTATTAAAT 1149
Qy 402 ProIleGlnTyrPheAenPheAlaAenLeuSerValPheSerIleGluSerLeuAlaArg 421
Db 1150 CCTGTAAACA---TTACAGTTTCATCTCGAGAGCTTTATAGAACAGAAATCAATTCGAGG 1206
Qy 422 IleTyrLeuGlyGlyThrGluAlaAenAenTyrIleThrSerGlnTyrGlyValSerArg 441
Db 1207 ATAAATATATCTTAACACTCTCTGTGAAT-----GGAGTACTCTGG 1248
Qy 442 ValIlePheAenThrSerAen---IleAenAenValProGlySerLeuArgTyrGluVal 460
Db 1249 GCTAGATTATTTGAGAAATCCCTGAATCTCTTAGAGGTAGCTTCTCTATATA 1308
Qy 461 ProAlaAen-----LeuProSerGlnThrIleLeuSerGluLeuPro 474
Db 1309 GGGTATACTGGAGTGGGACACAACATATTGTATTCAGAACT-----GAATATACA 1359
Qy 475 GlyLysAspLysProArgProAenAlaGlyAspPheSerHisArgLeuSerTyrIleSer 494
Db 1360 CCAGAAACAACAGACGACCAAAATATGAATCTTACAGTCAATAGATTATCTAATATA--- 1416
Qy 495 AenPheAspAlaArgArgSerSerGlyGlyIleValSerLeuLeuThrPheGlyTyr 514
Db 1417 -----AGACTAATATCAGGAACACCTTTGAGAGCACCATGATATATCTTGG 1461
Qy 515 AlaHisThrSerMetAspArgAenAenArgLeuGluProAspLysIleThrGlnIleAsp 534
Db 1462 AGCCACCGTAGTGCAGATCGTACAAATACCAATTAGTTCAGATAGCATTAACACAAATACA 1521
Qy 535 AlaValLysGlyTyrTrpGlyAenIleGlyPheValIle-----ProGlyProThr 551
Db 1522 TTGGTAAATCAATCAACCTTAATTCAGGTACTCTGTAGTCAGTGGGCCAGGATTTACA 1581
Qy 552 GlyGlyAenLeuValLysValSerAspSerTrpHisSerLeuLysValGlnAlaProGln 571
Db 1582 GGAGGGGATATATCCGAACACTAACGTTTATGTAGTACTAAGTATGGGTCTTAATTTT 1641
Qy 572 ArgGlnThrSer-----TyrArgIleArgLeuArgTyrAlaCysLeuValThrHis 588
Db 1642 AATAATACATCATTAACAGCGGTATCGGTGAGAGTTGCTTATGCTGCTTCTCAACAATG 1701
Qy 589 GlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCys 608
Db 1702 -----GTCCTGAGGGTAACTGTCGAGGAGGAGTACTATTTTGTATCAAGGATTCCTAGT 1755

Qy 609 SerAenSerSerGlyArgProSerAenThrLeuLeuGluSerAspPheArgTyrIleAsp 628
Db 1756 ACTATGAGTGCA-----AATGAGTCTTTGACATCTCAATCATTTAGATTGCGAGAA 1806
Qy 629 ValPro-----GlyIlePheThrProSerIleAenProLeuIleArg 642
Db 1807 TTTCTGTAGGTATTAGTGCACTCTGGCAGTCAAACTGCTGGAATTAAGTATAATATAAT 1866
Qy 643 TyrArgThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAen 662
Db 1867 GCAGGTAGACAAACGTTT-----CACTTGTATAAATTTGAATTCATTCGATTAAT 1917
Qy 663 ---ThrPheProAenGln---SerLeuGluLysArgGluGlnGluValAenAspLeuPhe 680
Db 1918 GCAACCTTCGAAGCAGAAATATGATTTAGAAAGAGCGCAAGAGCGGTGAATGCTCTGTTT 1977
Qy 681 IleAen 682
Db 1978 ACTAAT 1983
RESULT 11
US-09-661-322A-62
; Sequence 62, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 62
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-661-322A-62
Alignment Scores:
Pred. No.: 6e-85 Length: 3684
Score: 894.00 Matches: 252
Percent Similarity: 50.6% Conservative: 103
Best Local Similarity: 35.9% Mismatches: 275
Query Match: 24.9% Indels: 72
DB: 3 Gaps: 24
US-10-782-096-2 (1-682) x US-09-661-322A-62 (1-3684)
Qy 7 LysAenGluTyrGluMetLeuAspAlaLeuArgIleAenSerAenMetSerAenCysTyr 26
Db 16 AAAAATGAGATGAATTAATAATGCTTTATGATTCAGCT---GTATCGAATCATTC 72
Qy 27 ProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAenThrAenTyrLysGlu 46
Db 73 GCACAAATGAATCTATCAACCGCATCTCGTATT-----GAGGAT 111
Qy 47 TrpLeuAenMetCysAspSerAenThrGlnPheIleGlyAspIleSerThrTyrSerSer 66
Db 112 AGCTTGTGTATAGCCGAGGGGAAC-----AATATCGATCCATTTGTTAGC 156
Qy 67 ProGluAlaIleLeuSerValArgAspAlaValLeuThrGlyIleAenSerValGlyThr 86
Db 157 -----GCATCAACAGTCCAAACGGGTATTAAACATAGCTGCTAG 195
Qy 87 IleLeuSerAenLeuGlyValProLeuAlaSerGlnSerPheGlyIleIleSerArgLeu 106
Db 196 ATACTAGGTGATTAGGCGGTACCGTTTGTGCAAAATAGCTAGTATTTTATAGTTTCTT 255

Qy	107	IleGlyIleIeuTrp---	AlaGlyProAspProPheGluAlaLeuMetValLeuValGlu	125
Db	256	GTTCGGTGAATTA	TGGCCCGCGGCGAGAGATCCTTGGGAAATTTTCTCTAGAACATGTCGAA	315
Qy	126	GluLeuIleIysLysSerIle	AspGlnArgValArgGluAsnAlaLeuArgGluLeuGlu	145
Db	316	CATCTTTATAAGACA	CAAGTAAGCAAGNAATACTAGGAGATACGGCTTGTCTGCATTAACA	375
Qy	146	GlyLeuGlnGlyIleMet	ArgLeuTyrGlnThrArgLeuGlnAlaTlpLeuValAsnLys	165
Db	376	GGTTTAGGAATTCCT	TTAGAGCCTATCAACAGTCACCTTGAGATTGGCTAGAAAACCGT	435
Qy	166	AsnAspAspAsnArgArgAla---	LeuValThrGlnTyrAlaIleValAspAsnPhePhe	184
Db	436	GATGATCAAGAAC	GAGAAGTGTTCTTTATACCCAATATATAGCCTTTAGAACCTTGATTTT	495
Qy	185	GluLysAsnMetProLysPhe	LysGluArgAsnPheGluIleLeuLeuLeuProValTyr	204
Db	496	CTTAATCGATCGCCGCT	TTTTCGCAATTTAGAAACCAAGAAGTTCCATTTAATATGGTATAT	555
Qy	205	AlaGlnAlaAlaAsnLeu	HisLeuIleLeuLeuArgAspAlaAspTyrPheGlyAlaGln	224
Db	556	GCTCRACTGCAAAATTT	TACACCTATTATTATGAGATGCCTCTCTTTTGGTAGTGAA	615
Qy	225	TrpGlnLeuGlyAspAsp	GluIleArgAspAsnTyrIleArgLeuGlnGlyLeuIleArg	244
Db	616	TTTGGGCTTACATCC	CAAGAAATTCACGTTATTATGAGCGCCCAAGTGGAAAAACGAGA	675
Qy	245	GluTyrLysAspHisCysIle	ThrPheTyrAsnGlnGlyLeuAsnGlnPheAsnArgSer	264
Db	676	GAATATTCTGATTTAT	TGCGCAAGATGCTATAATAACGGGTTTAAATAATTTGAGAGGGACA	735
Qy	265	AsnAlaGlnAspTlpVal	SerPheAsnArgPheArgThrAspMetThrLeuThrValLeu	284
Db	736	AATGCTGAAAGTTGG	TTTCGCGATATAATCAATTCGCTAGAGACTTAAACGCTAGGAGTATTA	795
Qy	285	AspLeuAlaIleLeuPhe	ProAsnTyrAspProArgArgTyrProLeuAlaValLysThr	304
Db	796	GAICTAGTGGCACTAT	TCCCAAGCTATGACACGGCTGTTATCCNATGAATACCAAGTGCT	855
Qy	305	GluLeuThrArgGluVal	TyrThrAspProValGlyPheThrGlyValLeuGluSerGly	324
Db	856	CAATTAACAAGAGAAAT	TTTATACAGATCCAATTCGGAGAACAAATGCA---CCTTCAGGA	912
Qy	325	GlyArgThrTyrProTlp	TyrAsnProAsnAsnThrThrPheThrAlaMetGluAsnAsn	344
Db	913	TTTGCAAGTAGCAAA	TGGTTTAATTAATATGACACCATCGTTTCTGCCATAGAGGCTGCC	972
Qy	345	AlaArgArgProSerTyr	ThrThrTripleuAsnArgIlePheValTyrThrArgThr	364
Db	973	GTTATTAGGCTCCG	CATCTACTTGTGATTTCCAGAACAGCTTACAAATTTTCAGC---GTA	1029
Qy	365	LeuGlyAsnMetSerAsp	ValArg-----AsnIleTrpGlyGlyHisThrLeuValGlu	382
Db	1030	TTAAGTCGATGGAG	TAATACTCAATATATGAATTTACTGGGTGGGACATAGACTGAATCG	1089
Qy	383	AsnGlyAsnAspGlySer	GluIleThrHisAsnPheGlyLysThrAsp---SerIleThr	401
Db	1090	CGAAACAATAAGGG	GGTCAITTAAGTACCTGGCACACCGGAAATACCAATCTTCTATTAAAT	1149
Qy	402	ProIleGlnTyrPheAsn	PheAlaAsnLeuSerValPheSerIleGluSerLeuAlaArg	421
Db	1150	CCTGTATACA---	TTACAGTTCCATCTCGAGACGCTTTATAGACAGAAATCATTTGCAAGG	1206
Qy	422	IleTyrLeuGlyGlyThr	GluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSerArg	441
Db	1207	ATAAATATACTTCT	TAACCTACTCTCTGTGAAT-----GGAGTACCTTGG	1248
Qy	442	ValIlePheAsnThrSer	Asn---IleAsnAsnValProGlySerLeuArgTyrGluVal	460
Db	1249	GCTAGATTTAAT	TGGAGAAATCCCGCTGAATTTCTCTAGAGTAGTACCTTCTCTATCATATA	1308

Qy	461	ProAlaAn-----LeuProSerGlnThrIleLeuSerGluLeuPro	474
Db	1309	GGGTATACTGGAGTGGGACACAACTATTATTGATTCAGAACT-----GAATTACCA	1359
Qy	475	GlyLyAspLybProArgProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSer	494
Db	1360	CCAGAACACAGNACGACCAAAATTATGAATCTTCAGTCATAGATTATCTAATATA---	1416
Qy	495	AsnPheAspAlaArgArgSerSerSerGlyGlyIleValSerLeuLeuThrPheGlyTyr	514
Db	1417	-----AGACTAATATCAGGAACACACTTTTGAGAGCACCAGTATATTCTTGG	1461
Qy	515	AlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspLybIleThrGlnIleAsp	534
Db	1462	ACGCACCGTATTGCAGATCGTACAAATACCAATTAGTTTCAGATAGCATAAACACAAATACCA	1521
Qy	535	AlaValLybGlyTyrGlyGlyAsnIleGlyPheValIle-----ProGlyProThr	551
Db	1522	TTGTAAATCAATTCAACTTAATTCAGGTACCTCTGTAGTCAGTGGCCGAGATTATACA	1581
Qy	552	GlyGlyAsnLeuValLybValSerAspSerTrpHisSerLeuLybValGlnAlaProGln	571
Db	1582	GGAGGGATATAATCCGAACCTAACGTTAATGGTAGTGTACTAAAGTAGGGCTTTAATTTT	1641
Qy	572	ArgGlnThrSer-----TyrArgIleArgLeuArgTyrAlaCysLeuValThrHis	588
Db	1642	AATAATACATCATTCACACGGGTATCGCGTCAGAGTTCGTTATGCTGCTCTCAACAACATG	1701
Qy	589	GlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPheAspCys	608
Db	1702	-----GTCCTGAGGGTAACCTGTCGGAGGAGTACTACTTTTGATCAAGGATTCCCTAGT	1755
Qy	609	SerAsnSerSerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAsp	628
Db	1756	ACTATGATGCA-----AATGAGTCTTCACATCTCAATCATTTAGATTTCGAGAA	1806
Qy	629	ValPro-----GlyIlePheThrProSerIleAsnProLeuIleArg	642
Db	1807	TTTCTCTAGTGATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATAAGTAATAAT	1866
Qy	643	TyrArgThrGlnSerPheGlyThrHisAlaIleAspLybPheGluPheIleProLeuAsn	662
Db	1867	GCAGGTAGACAAACGTTT-----CACTTTGATATAAATTGAATTCATTCCAATTACT	1917
Qy	663	---ThrPheAsnGln---SerLeuGlyLybArgGluGlnGluValAsnAspPhe	680
Db	1918	GCAACCTTCGAGCAGAAATATGATTAGAAAGACGCGCAGAGCGGTGAATGCTCTGTTT	1977
Qy	681	IleAsn	682
Db	1978	ACTAAT	1983

RESULT 12

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US-09-053-549-1
; Sequence 1, Application US/09053549
; Patent No. 6121521
; GENERAL INFORMATION:
; APPLICANT: Desai, Nalini
; TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121521artis Corporation
; STREET: 3054 Cornwallis Rd.
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/053,549
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..3694
; OTHER INFORMATION: /product= "hyFF"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 8854
; OTHER INFORMATION: /note= "Sequence"
; Patent No. 6121521
; OTHER INFORMATION: containing cod
; US-09-053-549-1

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Db 1514 ATCCCATGGTGAAGCCAGCGAGCTGCCCGGCGGCCACCCAGCGTGGTGGCGGCCCGCGC 1573
QY 550 ProThrGlyGlyAsnLeuValSerAspSerTrpHis-----SerLeu 565
Db 1574 TTCACGGCGGCGACATCTGGCGCGCACCAACCGCGGGCTTCGGCCCCATCCGCGTG 1633
QY 566 LysValGlnAlaProGlnArgGlnThrSerTyArgileArgLeuArgTyAlaCysLeu 585
Db 1634 ACCGTGAACGGCCCTGACCAG---CCCTACCGCATCGGCTTCGGCTACCGCAGCAC 1690
QY 586 ValThrHisGlyAspAlaIlePheValGluHisSerGlySerSer---HisIleValSer 604
Db 1691 GTGACTTCGAC-----TTCCTGGTGGAGCGCGCGGCCACCAACCGTGAACAACCTCCGC 1744
QY 605 PhePheAspCysSerAsnSerSerGlyArgProSerAsnThrLeuGluSerAspPhe 624
Db 1745 TTCCTGGCGCACCATGAACAGC-----GGCGACGAGCTGAAGTACGGCAACTTC 1792
QY 625 -----ArgTyIleAspValProGlyIlePheThrProSerIleAsnProLeuIleArg 642
Db 1793 GTGCGCGCGCCCTTACCACCCCTTCACCTTCACC---CAGATCAGAACATCATCCGC 1849
QY 643 TyrArgThrGlnSerPhe-----GlyThrHisAlaIleAspLysPheGluPheIle 659
Db 1850 ACCAGCATCCAGGCGCTGAGCGCAACGCGAGGTGTATCATCGACAAGATCGAGATCATC 1909
QY 660 ProLeuAsn---ThrPheProAsnGln---SerLeuGluLysArgGluGlnGluValAsn 677
Db 1910 CCGGTGACTGCCACCTTCGAGCGCGAGTATGATCGCTGGAGCGGCCCGAGGCGCGTGAC 1969
QY 678 AspLeuPheIleAsn 682
Db 1970 GCCCTGTTCCACCAAC 1984

RESULT 13

US-09-178-252-22
; Sequence 22, Application US/09178252
; Patent No. 6218198
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; CURRENT APPLICATION NUMBER: US/09/178,252
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/065,215
; EARLIER FILING DATE: 1997-11-12
; EARLIER APPLICATION NUMBER: 60/076,445
; EARLIER FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 3558
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-178-252-22

Alignment Scores:

Pred. No.:	1,958-84	Length:	3558
Score:	889.00	Matches:	251
Percent Similarity:	50.7%	Conservative:	104
Best Local Similarity:	35.9%	Mismatches:	273
Query Match:	24.7%	Indels:	72
DB:	3	Gaps:	24

US-10-782-096-2 (1-682) x US-09-178-252-22 (1-3558)

QY 7 LysAsnGluTyGluMetLeuAspAlaLeuArgIleAsnSerAsnMetSerAsnCysTy 26
Db 16 AAGACGAGACGAGATCATCAACGCTCTTTCTATCCAGCT---GTTTCTAACCATTTCT 72

QY 27 ProArgTyProLeuAlaLysAspProGlnMetThrMetArgAsnThrAsnTyLysGlu 46
Db 73 GCTCAGATGAACTTTCTACTGATGCTAGATC-----GAGGAT 111
QY 47 TrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSerThrTySerSer 66
Db 112 TCTCTTTCATTCGTGAGGGAAC-----AACATTGATCCATTCGTTCT 156
QY 67 ProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIleAsnSerValGlyThr 86
Db 157 -----GCTTCTACTGTTCAAACCTGGAATCAACATTCGCTGAAGA 195
QY 87 IleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGlyIleIleSerArgLeu 106
Db 196 ATCTCTGGAGTTCTGGAGTTCCATTCGCTGGACAGATGCTCTTTCTTACTCTTTCCCT 255
QY 107 IleGlyIleLeuTIP---AlaGlyProAspProPheGluAlaLeuMetValLeuValGlu 125
Db 256 GTTGGAGAGCTTTGGCTTAGGGAAGAGATCTCTGGAGATCTTCTTGAGCATGTTGAG 315
QY 126 GluLeuIleLysLysSerIleAspGlnArgValArgGluAsnAlaLeuArgGluLeuGlu 145
Db 316 CAGTTGATTGCTCAACAAGTTACTCGAAACACTAGAGATACTGCTCTTGCTAGACTCAA 375
QY 146 GlyLeuGlnGlyIleMetArgLeuTyGlnThrArgLeuGlnAlaTrpLeuValAsnLys 165
Db 376 GGACTTGGAAACTCTTTTCAGAGCTTACCACAACATCTCTTGAGGATGGCTTGAGAACAGA 435
QY 166 AsnAspAspAsnArgAlaAla---LeuValThrGlnTyAlaIleValAspAsnPhePhe 184
Db 436 GATGATGCTAGNACTAGATCTGTGTTGACTACTGATGCTTCTTGAGCTTGACTTC 495
QY 185 GluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeuLeuProValTy 204
Db 496 TTGAACGCTATGCCATTGTCGTATCAGAACCAAGAGTTCCACTTCTCATCGTGTAC 555
QY 205 AlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAlaAspTyPheGlyAlaGln 224
Db 556 GCTCAAGCTGCTAACCTTCATCTTCTTCTTAGAGATGCTAGTGTGTCGGATCTGAG 615
QY 225 TrpGlnLeuGlyAspAspGluIleArgAspAsnTyIleArgLeuGlnGlyLeuIleArg 244
Db 616 TTCGCACTTCTTCAAGAGATTCAAAGATATACGAGAGACAAGTTGAGAGAGACTAGA 675
QY 245 GluTyLysAspHisCysIleThrPheTyArgGlnGlyLeuAsnGlnPheAsnArgSer 264
Db 676 GAGTACTCTGACTACTGGCTAGGTGGTACAACACTGGATTGAACAACCTTAGAGGAACT 735
QY 265 AsnAlaGlnAspTTPValSerPheAsnArgPheArgThrAspMetThrLeuThrValLeu 284
Db 736 AACGCTGAGTCTTGGCTTAGATACCAACAGTTCCAGAGAGATCTTACTCTTGGAGTTCT 795
QY 285 AspLeuAlaIleLeuPheProAsnTyArgProArgArgTyProLeuAlaValLysThr 304
Db 796 GATCTGTGCTGCTTCCATCTTACCATCTAGAGTGTACCTTATGACACTTCTGCT 855
QY 305 GluLeuThrArgGluValTyThrAspProValGlyPheThrGlyValLeuGluSerGly 324
Db 856 CAACCTTACTAGAGATCTACACTGATCCAATCGGAAGAACTAACGCT---CCAATCTGA 912
QY 325 GlyArgThrTyProTTPTyAsnProAsnAsnThrPheThrAlaMetGluAsnAsn 344
Db 913 TTCGCTTCTACTAATCTGTTCAACAACACGCTCCATCTTCTCTGCTGAGCGGTGCA 972
QY 345 AlaArgArgArgProSerTyThrThrTrpLeuAsnArgIlePheValTyThrArgThr 364
Db 973 GTGATCAGACCCACATCTTCTTGACTTCCAGAGCAACTTACTATCTTCTCT---GTT 1029
QY 365 LeuGlyAsnMetSerAspValArg-----AsnIleTrpGlyGlyHisThrLeuValGlu 382
Db 1030 CTTTCTAGATGCTCTAACACTCAGTACATGAACTACTCTGGTTGGACATAGACTTGAGTCT 1089

383 AsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyIleThrAsp---SerIleThr 401
Db AGAACTATCAGAGGATCTCTTCTACTCTACTGGAACACATCAACTCTTATCAAC 1149
402 ProIleGlnTyPheAsnPheAlaAsnLeuSerValPheSerIleGluSerLeuAlaArg 421
Db CAGATTACT---CTTCAGTTCTACTCTAGAGATGTGTACAGACGAGTCTTTCGTGGA 1206
422 IleTyrLeuGlyGlyThrGluAlaAsnAntyIleThrSerGlnTyGlyValSerArg 441
Db ATCAACATCTCTTACTACTCTCAGTGAAC-----GGAGTTCTCTGG 1248
442 ValIlePheAsnThrSerAsn---IleAsnAsnValProGlySerIleuArgTyrGluVal 460
Db GCTAGATCAACTGGAGAACCCATCGAATCTCTTAGAGGTTCCTTGTGTACACATT 1308
461 ProAlaAsn-----LeuProSerGlnThrIleLeuSerGluLeuPro 474
Db CGATACACTGGAGTTGGTACCAGTTGTCGATTCGAGACT-----GAGCTTCCA 1359
475 GlyLysAspLysProArgProAsnAlaGlyAspPheSerHisArgLeuSerTyIleSer 494
Db CCAGAGACTACTGAGAGACCAAACTACGAGTCTTACTCTCATAGACTTCTTAACATT--- 1416
495 AsnPheAspAlaArgArgSerSerGlyIleValSerLeuLeuThrPheGlyTyr 514
Db -----CGTTGATCTCTGGAACACTCTTAGAGCTCCAGTCTACTCTTGG 1461
515 AlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspLysIleThrGlnIleAsp 534
Db ACTCATAGATCTGCTGATAGAACTAAACACATCTCTTCTGATCTTATCACTCAGATTCCA 1521
535 AlaValLysGlyTyrGlyGlyAsnIleGlyPheValIle-----ProGlyProThr 551
Db CTGTGAGTCTTCAACTGGAATCTCGAATCTCGTTGTTCTCGACACGAGATTCACT 1581
552 GlyGlyAsnLeuValLysValSerAspSerTrpHisSerLeuLysValGlnAlaProGln 571
Db GGAGAGACATCATCAGAACTAAACGTGAACGGATCTGTTCTTCTATGGGATTGAATTC 1641
572 ArgGlnThrSer-----TyrArgIleArgLeuArgTyrAlaCysLeuValThrHis 588
Db ACAACACTTCTCTTCAAGATACAGATTAGATTAGATACGCTCTTCAAACTATG 1701
589 GlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPheAspCys 608
Db -----GTTCTTAGATTACTGTGGAGGATCTACTTCTCGATCAAGGATTCCTACT 1755
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643 TyrArgThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn 662
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663 ----ThrPheProAsnGlnSer---LeuGluLysArgGluGlnGluValAsnAspLeuPhe 680
Db GCTACTCTCGAGCAGAGTCTGACTTGGAAAGACGACAGAGCGGTGAATGCTCTGTTTC 1977

RESULT 14

US-09-826-660-22
; Sequence 22, Application US/09826660
; Patent No. 6673990
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins

FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 3558
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-22

Alignment Scores:
Pred. No.: 1.95e-84 Length: 3558
Score: 889.00 Matches: 251
Percent Similarity: 50.7% Conservative: 104
Best Local Similarity: 35.9% Mismatches: 273
Query Match: 24.7% Indels: 72
DB: 3 Gaps: 24

US-10-782-096-2 (1-682) x US-09-826-660-22 (1-3558)

QY 7 LysAsnGlyTyGluMetLeuAspAlaLeuArgIleAsnSerAsnMetSerAsnCytyr 26
Db 16 AAGAACGAGACGAGATCATCAACGCTCTTATCCCCAGCT---GTTTCAACCATCT 72
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Db 73 GTCAGATCAACTTCTTACTGATGTAGAATC-----GAGGAT 111
QY 47 TrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSerThrTyrSerSer 66
Db 112 TCTCTTGGCATTTGCTGAGGGAAC-----AACATTGATCATTTCTGTTTCT 156
QY 67 ProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIleAsnSerValGlyThr 86
Db 157 -----GCTTCTACTGTTTCAAACTGGAATCAACATTCGTGGAAGA 195
QY 87 IleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGlyIleIleSerArgLeu 106
Db 196 ATCTCTGGAGTCTTGGAGTTCATTCGCTGGACAGATTGCTTCTTCTACITCTTCCIT 255
QY 107 IleGlyIleLeuTyr---AlaGlyProAspProPheGluAlaLeuMetValLeuValGlu 125
Db 256 GTTGGAGAGCTTTGGCTAGGGGAAGAGATCCTTGGAGATCTTCTTGGAGCATGTTGAG 315
QY 126 GluLeuIleLysLysSerIleAspGlnArgValArgGluAsnAlaLeuArgGluLeuGlu 145
Db 316 CAGTTGATTCGTCACAAAGTCTTACTAGAACACTAGAGATACGCTCTTCTAGACTCAA 375
QY 146 GlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGlnAlaIleTrpLeuValAsnLys 165
Db 376 GGACTTGGAACTCTTTCAGACTTACCAACAATCTCTTGAGATTGGCTTGGAGACAGA 435
QY 166 AsnAspAspAsnArgArgAla---LeuValThrGlnTyrAlaIleValAspAsnPhePhe 184
Db 436 GATGATGCTAGAACTAGATCTGTGTTGTACACTCAGTACATGCTCTTGGAGCTTACTTC 495
QY 185 GluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeuProValTyr 204
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QY 205 AlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAlaAspTyrPheGlyAlaGln 224
Db 556 GCTCAGCTGCTAACCTTCTTCTTCTTCTTAGAGATGCTAGCTTGTTCGATCTGAG 615

Qy 225 TrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArgLeuGlnGlyLeuValArg 244
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Qy 245 GluTyrIysAspHisCyelleThrPheTyrAsnGlnGlyLeuAsnGlnPheAsnArgSer 264
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796 GATCTTGTGCCTGTTGCCATCTCCATCTACGATACTAGAGTGTACCATGAACACTTCTGCT 855

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Qy 325 GlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPheThrAlaMetGluAsnAsn 344
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Qy 345 AlaArgArgProSerfYrThrThrTrpLeuAsnArgIlePheValTyrThrArgThr 364
Dbb : : : : :
973 GTGATCAGACCAACCATCTCTTGAGCTTCCAGAGCAACTTACTACTTCTCTCT---GTT 1029

Qy 365 LeuGlyAsnMetSerAspValArg-----AsnIleTrpGlyGlyHisThrLeuValGlu 382
Dbb : : : : :
1030 CTTTCTAGATGGTCTAAACACTCAGTACATGAACACTACTGGGTGGACATAGACTTGAGTCT 1089

Qy 383 AsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyLysThrAsp---SerIleThr 401
Dbb : : : : :
1090 AGAACTATCAGAGATCTCTTCTACTCTTACTCATGGAACAACATACTTCTATCAAC 1149

Qy 402 ProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIleGluSerLeuAlaArg 421
Dbb : : : : :
1150 CCAGTTACT--CTTCAGTTTCACTTCTAGAGATGTGTACAGAACTGAGTCTTTCGCTGGA 1206

Qy 422 IleTyrLeuGlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSerArg 441
Dbb : : : : :
1207 ATCAACATCTTCTTACTACTCCAGTGAAC-----GGAGTCTCTGG 1248

Qy 442 ValIlePheAsnThrSerAsn---IleAsnAsnValProGlySerLeuArgTyrGluVal 460
Dbb : : : : :
1249 GCTAGATTCACTGGAGAAACCCATCGAACTCTCTAGAGTTCTTGTGTACACCAATT 1308

Qy 461 ProAlaAsn-----LeuProSerGlnThrIleLeuSerGluLeuPro 474
Dbb : : : : :
1309 GGATACACTGGAGTTGGTACCAGTTCTTCGATTCTGAGACT-----GAGCTTCCA 1359

Qy 475 GlyIysAspLysProArgProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSer 494
Dbb : : : : :
1360 CCAGAGACTACTCGAGAGACCAAACCTACGAGTCTTACTCTCATGACTTTCTAACATTT-- 1416

Qy 495 AsnPheAspAlaArgSerSerSerGlyGlyIleValSerLeuLeuThrPheGlyTrp 514
Dbb : : : : :
1417 -----CSTTTGATCTCTGGAAAACACTCTTAGAGCTCCAGTGTGATCTCTGG 1461

Qy 515 AlaHisThrSerMetAspArgAsnAsnArgLeuGluProAspLysIleThrGinIleAsp 534
Dbb : : : : :
1462 ACTATAGATCTGCTGATAGAACTAAACACCATCTCTTCTGATTCTATCACTCAGATTCCA 1521

Qy 535 AlavalysGlyTrpGlyGlyAsnIleGlyPheValIle-----ProGlyProThr 551
Dbb : : : : :
1522 CTTGTGAAGTCTTTCAACTTGAACCTCTCGAACTTCTGTTGTTCTGACCAAGGATTCAC 1581

Qy 552 GlyGlyAsnLeuValLysValSerAspSerTrpHisSerLeuLysValGlnAlaProGln 571
Dbb : : : : :
1582 GGAGGACACATCATCAGAACTAAACGTGAACGGATCTCTTCTTCTAGGGATGAACCTC 1641

Qy 572 ArgGlnThrSer-----TyrArgIleArgLeuArgTyrAlaCysLeuValThrHis 588

Db	1642	AAACAACACTTCTCTTCAAGATACAGAGTAGAGTTAGATACGCTCTTCTCAAACTATG	1701
Qy	589	GlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCys	608
Db	1702	-----GTTCCTTAGAGTTACTGTTGGAGGATCTACTACTTTTCGATCAAGGATTCCTCATCT	1755
Qy	609	SerAsnSerSerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAsp	628
Db	1756	ACTATGCTGCT-----AACGAGTCTCTTACTTCTCAATCTTTTCAGATTCGCTGAG	1806
Qy	629	ValPro-----GlyIlePheThrProSerIleAsnProLeuIleArg	642
Db	1807	TTCCCAAGTTGGAAATCTCTGCTCTGGATCTCAAACTGCTGGAATCTCTATCTCTAAACAAC	1866
Qy	643	TyrArgThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn	662
Db	1867	GCTGGGAAGACAACTTTC-----CACTTCGACAAGATTGAGTTCATTCCAATCACT	1917
Qy	663	---ThrPheProAsnGlnSer---LeuGluLysArgGluGlnGluValAsnAspLeuPhe	680
Db	1918	GCTACTCTCGAGCGAGTCTGACTTGGAAAGAGCACAGAAGCGGTGAATGCTCTGTTTC	1977
RESULT 15			
US-08-377-690-1			
; Sequence 1, Application US/08377690			
; Patent No. 5628995			
; GENERAL INFORMATION:			
; APPLICANT: PEPEROEN, Marnix			
; APPLICANT: JANSSEN, Stefan			
; APPLICANT: DENOLF, Peter			
; TITLE OF INVENTION: CONTROL OF OSTRINIA			
; NUMBER OF SEQUENCES: 3			
; CORRESPONDENCE ADDRES:			
; ADDRESSEE: Burns, Doane, Swecker & Mathis			
; STREET: The George Mason Bldg., Washington & Prince			
; STREET: Sts.			
; CITY: Alexandria			
; STATE: Virginia			
; COUNTRY: United States			
; ZIP: 22313-1404			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/377,690			
; FILING DATE:			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US/08/164,781			
; FILING DATE:			
; APPLICATION NUMBER: US 07/938,362			
; FILING DATE: 31-AUG-1992			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Crane-Feury, Sharon E			
; REGISTRATION NUMBER: 36,113			
; REFERENCE/DOCKET NUMBER: 010830-039			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (703) 836-6620			
; TELEFAX: (703) 836-2021			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 4074 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA (genomic)			
; ORIGINAL SOURCE:			
; ORGANISM: Bacillus thuringiensis			
; STRAIN: entomocidus HD 110			
; FEATURE:			

; NAME/KEY: CDS
 ; LOCATION: 186..3872
 ; OTHER INFORMATION: /note= "PROPERTIES: CryIB is toxic to
 ; OTHER INFORMATION: Ostrinea nubilalis (among others)"
 ; US-08-377-690-1

Alignment Scores:

Pred. No.: 4,48e-84 Length: 4074
 Score: 886.50 Matches: 249
 Percent Similarity: 50.1% Conservative: 102
 Best Local Similarity: 35.5% Mismatches: 277
 Query Match: 24.6% Indels: 73
 DB: 2 Gaps: 25

US-10-782-096-2 (1-682) x US-08-377-690-1 (1-4074)

QY 7 LysAsnGluTyrGluMetLeuAspAlaLeuAlyGleAsnSerAsnMetSerAsnCysTyr 26
 DB 201 AAAAATGAGAAATTAATGCTGATCGAATCATCCGCACAAATGATCTATTA 260
 QY 27 ProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThrAsnTyrLysGlu 46
 DB 261 CCA-----GATCGTGTATTGAGGAT 281
 QY 47 TrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSerThrTyrSerSer 66
 DB 282 AGCTTGATGATAGCCGAGGGGAAC-----AATATTGATCCATTGTTAGC 326
 QY 67 ProGluAlaLeuSerValArgAspAlaValLeuThrGlyLeuAsnSerValGlyThr 86
 DB 327 -----GCATCAACAGTCCAAACGGGTATTAAACATAGCTGTAGTA 365
 QY 87 IleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGlyIleIleSerArgLeu 106
 DB 366 ATACTAGGCGTATTGGCGCTACCGTTGCTGGACACTAGTAGTATTTTATAGTTTCTT 425
 QY 107 IleGlyIleLeuTrp---AlaGlyProAspProPheGluAlaLeuMetValLeuValGlu 125
 DB 426 GTTGGTGAATTTATGGCCCGCGCAGAGATCGATGGGAAATTTTCTAGAACATGTCGAA 485
 QY 126 GluLeuIleLysSerIleAspGlnArgValArgGluAsnAlaLeuArgGluLeuGlu 145
 DB 486 CAACCTTATAAACAACAAATAACAGAAATGCTAGGAATACCGCTCTTCTCGATTACAA 545
 QY 146 GlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGlnAlaTrpLeuValAsnLys 165
 DB 546 GGTTTAGGAGATTCCTTCAGACCTATCAACAGTCACTTGAAGATTGGCTAGAAACCGT 605
 QY 166 AsnAspAspAsnArgAlaLeuVal---ThrGlnTyrAlaIleValAspAsnPhePhe 184
 DB 606 GATGATGCAAGAACGAGAGATGTTCTTCATACCAATATATAGCTTTAGAACTTGATTTT 665
 QY 185 GluLysAsnMetProLysPheLysGluArgAsnPheGluIleLeuLeuLeuProValTyr 204
 DB 666 CTTAATGCGATCCGCTTTTCGCAATTAGAAACCAAGAGTTCCCAATTATTGATGTATAT 725
 QY 205 AlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAlaAspTyrPheGlyAlaGln 224
 DB 726 GCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCTCTCTTTTGGTAGTAA 785
 QY 225 TrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArgLeuGlnGlyLeuLeuArg 244
 DB 786 TTTGGGCTTACATCGCAGGAAATTCACCGCTATTATGAGCGCAAGTGGAAACGACGAGA 845
 QY 245 GluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeuAsnGlnPheAsnArgSer 264
 DB 846 GATTATTCCGACTATTTCGCTAGAAATGGTATATATACAGGTCTAAATAGCTTTGAGAGGACA 905
 QY 265 AsnAlaGlnAspTrpValSerPheAsnArgPheAspThrAspMetThrLeuThrValLeu 284
 DB 906 AATGCCGCAAGTTGGTACGGTATTATATCAATTCCTGAGAGATCTTAACGTTAGAGTATTA 965
 QY 285 AspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyrProLeuAlaValLysThr 304

DB 966 GATCTAGTGGCACTATTCCAAAGCTATGACACTCGCACTTATCCCAATTAATACGAGTGCT 1025
 QY 305 GluLeuThrArgGluValTyrThrAspProValGlyPheThrGlyValLeuGluSerGly 324
 DB 1026 CAGTTAACAGAGAGATTATACAGACGCAATTTGGAGCAACAGGGTA-----AAT 1076
 QY 325 GlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPheThrAlaMetGluAsnAsn 344
 DB 1077 ATGGCAAGTATGAATTTGGTATATAATAATATGACCTTCGTTCTCTGCCATAGAGGCTGCG 1136
 QY 345 AlaArgAspArgProSerTyrThrTrpLeuAsnArgIlePheValTyrThrArgThr 364
 DB 1137 GCTATCCGAAGCCGCACTACTTGTATTTCTAGAACAACTTACAAATTTTTCGCGCTTCA 1196
 QY 365 LeuGlyAsnMetSerAspValArgAsnIle-----TrpGlyGlyHisThrLeuValGlu 382
 DB 1197 ---TCACGATGAGTAATACTAGGCATATGACTTATTGGCGGGGCACAGATTCAATCT 1253
 QY 383 AsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyLysThrAsp---SerIleThr 401
 DB 1254 CGGCCAATAGGAGGGCGGATTAATAATACCTCAACGCATGGGGCTACCAATACTTCTAATA 1313
 QY 402 ProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIleGluSerLeuAlaArg 421
 DB 1314 CCGTGAACA---TTACGGTTCGCATCTCGAGACGTTTATAGGATGGAATCATATGCAGGA 1370
 QY 422 IleTyrLeuGlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSerArg 441
 DB 1371 GTGCTCTATGGGAAT-----TACCTTGAACCTATTCTCGTGTCCTACT 1418
 QY 442 ValIlePheAsnThrSerAsnIleAsnValPro-----GlySerLeuArgTyrGlu 459
 DB 1419 GTTAGGTTTAAATTTACGAACCTCAGAAATATTCTGATAGAGGTACCGCTAACTATAGT 1478
 QY 460 ValProAlaAsnLeuProSerGlnThrIleLeu-----SerGluLeuProGlyLys 476
 DB 1479 CAACCTTATAGTCACTCGGCTTCAATTTAAAGATTTCAGAAACTGAATTTACCACAGAA 1538
 QY 477 AspLysProArgProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPhe 496
 DB 1539 ACACAGAACGACCAATTTATCACTTACAGTTCACAGTTTATCTCATATAGGTATAT 1598
 QY 497 AspAlaArgArgSerSerSerGlyIleValSerLeuLeuThrPheGlyTrpAlaHis 516
 DB 1599 TTACAATCCAGG-----GTGAATGTACCGTATATTCTTGGACGCAT 1640
 QY 517 ThrSerMetAspArgAsnAsnArgLeuGluProAspLysIleThrGlnIleAspAlaVal 536
 DB 1641 CGTAGTCGAGATCGTACGAATACGATTGGACCAAAATAGAAATCACCACAAATCCCAATGGTA 1700
 QY 537 LysGlyTrpGlyGlyAsnIleGlyPheValIle-----ProGlyProThrGlyGly 553
 DB 1701 AAAGCATCGCACTTCTCAAGGTACCACTGTGTAGAGGACGAGATTCTTCTGTGGG 1760
 QY 554 AsnLeuValLysValSerAspSerTrpHis-----SerLeuLysValGlnAla 569
 DB 1761 GATATTTCTCGAAGAACGAATACTCGTGTGATTGGACCGATAAGAGTAACGTGTAACGGA 1820
 QY 570 ProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGly 589
 DB 1821 CCATTAACACACA---AGATATCGTATAGGATTCGCTATGCTTCAACTGTAGATTGTAT 1877
 QY 590 AspAlaIlePheValGluHisSerGlySerSer---HisIleValSerPheAspCys 608
 DB 1878 -----TCTTTGTATCAGTCGAGGAGTACTACTGTAAATAATTTTAGATTCTCTACGTACA 1931
 QY 609 SerAsnSerSerGlyArgProSerAsnThrLeuLeuGluSerAspPhe-----ArgTyr 626
 DB 1932 ATGNACAGT-----GGAGACGAACTAAATAACGGAATTTTGTGAGACGCTGCT 1979
 QY 627 IleAspValProGlyIlePheThrProSerIleAsnProLeuIleArgTyrArgThrGln 646

Db 1980 TTTACTACACCTTTTACTTTTACA---CAAATTCAAGATATTAATTCGAACGTCCTATTCAA 2036
Qy 647 SerPhe-----GlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 2037 GGCCTTAGTGGAAATGGGGAAGCTGTATATAGATAAAATTGAAATTTATTCAGTTACTGCA 2096
Qy 663 ThrPheProAsnGln---SerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
Db 2097 ACCTTCGAAGCAGAAATATGATTTAGAAAGAGCGCGGCGTGAATGCTCTGTTTACT 2156
Qy 682 Asn 682
Db 2157 AAT 2159

Search completed: January 21, 2006, 04:00:20
Job time : 391 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: January 20, 2006, 23:03:47 ; Search time 1397 Seconds
(without alignments)
4037.019 Million cell updates/sec
Title: US-10-782-096-2
Perfect score: 3597
Sequence: 1 MNSYKKNKBYEMLDALRINS.....TFPNOSLEKREQVNDLFN 682
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-O=/cgn2_1/USPTO_spool/US10782096/runat_20012006_095216_24424/app_query.fasta_1.839
-DB=Published Applications/NA_Main_QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=spt
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10782096 @CGN 1.1 1026 @runat_20012006_095216_24424 -NCPU=6 -ICPU=3
-NO_WMAP -NEG SCORES=0 -WAIT -DSFBLOCK=100 -DEV TIMEOUT=120 -WARN TIMEOUT=30
-THREADS=1 -XGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	26.4	3621	5	US-10-032-717-1
2	948	26.4	3621	6	US-10-414-637-1
3	948	26.4	3621	7	US-10-606-320-1
4	948	26.4	3621	8	US-10-746-914-1
5	948	26.4	3621	10	US-11-021-115-5
6	948	26.4	4874	5	US-10-032-717-27
7	948	26.4	4874	6	US-10-414-637-27

8	948	26.4	4874	7	US-10-606-320-17	Sequence 17, Appl
9	948	26.4	4874	8	US-10-746-914-17	Sequence 17, Appl
10	940.5	26.1	3504	5	US-10-089-678-2	Sequence 2, Appl
11	940.5	26.1	3690	5	US-10-089-678-3	Sequence 3, Appl
12	926	25.7	2003	5	US-10-032-717-5	Sequence 5, Appl
13	926	25.7	2003	6	US-10-414-637-5	Sequence 5, Appl
14	926	25.7	2010	5	US-10-032-717-9	Sequence 9, Appl
15	926	25.7	2010	5	US-10-032-717-15	Sequence 15, Appl
16	926	25.7	2010	6	US-10-414-637-9	Sequence 9, Appl
17	926	25.7	2010	6	US-10-414-637-15	Sequence 15, Appl
18	926	25.7	2010	7	US-10-606-320-5	Sequence 5, Appl
19	926	25.7	2010	7	US-10-606-320-11	Sequence 11, Appl
20	926	25.7	2010	8	US-10-746-914-5	Sequence 11, Appl
21	926	25.7	2010	8	US-10-746-914-11	Sequence 11, Appl
22	925.5	25.7	2022	7	US-10-606-320-49	Sequence 49, Appl
23	925.5	25.7	2022	7	US-10-606-320-81	Sequence 81, Appl
24	925.5	25.7	2022	8	US-10-746-914-49	Sequence 49, Appl
25	925.5	25.7	2022	8	US-10-746-914-81	Sequence 81, Appl
26	925	25.7	2022	5	US-10-032-717-11	Sequence 11, Appl
27	925	25.7	2022	6	US-10-414-637-11	Sequence 11, Appl
28	925	25.7	2022	7	US-10-606-320-7	Sequence 7, Appl
29	925	25.7	2022	7	US-10-606-320-25	Sequence 25, Appl
30	925	25.7	2022	7	US-10-606-320-29	Sequence 29, Appl
31	925	25.7	2022	7	US-10-606-320-33	Sequence 33, Appl
32	925	25.7	2022	7	US-10-606-320-69	Sequence 69, Appl
33	925	25.7	2022	8	US-10-746-914-7	Sequence 7, Appl
34	925	25.7	2022	8	US-10-746-914-25	Sequence 25, Appl
35	925	25.7	2022	8	US-10-746-914-29	Sequence 29, Appl
36	925	25.7	2022	8	US-10-746-914-33	Sequence 33, Appl
37	925	25.7	2022	8	US-10-746-914-69	Sequence 69, Appl
38	924.5	25.7	2022	7	US-10-606-320-43	Sequence 43, Appl
39	924.5	25.7	2022	7	US-10-606-320-75	Sequence 75, Appl
40	924.5	25.7	2022	8	US-10-746-914-43	Sequence 43, Appl
41	924.5	25.7	2022	8	US-10-746-914-75	Sequence 75, Appl
42	924	25.7	2025	7	US-10-606-320-45	Sequence 45, Appl
43	924	25.7	2025	7	US-10-606-320-77	Sequence 77, Appl
44	924	25.7	2025	8	US-10-746-914-45	Sequence 45, Appl
45	924	25.7	2025	8	US-10-746-914-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-10-032-717-1
; Sequence 1, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry1218-1
US-10-032-717-1

Alignment Scores:				
Pred. No.:	3 04e-96	Length:	3621	
Score:	948.00	Matches:	248	
Percent Similarity:	50.9%	Conservative:	119	
Best Local Similarity:	34.4%	Mismatches:	276	
Query Match:	26.4%	Indels:	78	
DB:	5	Gaps:	25	
US-10-782-096-2 (1-682) x US-10-032-717-1 (1-3621)				
QY	3	SerTyrLysAsnGluTrpGluMetLeuAspAlaLeuArgIleAsnSerAsnMet	22	
DB	4	AGTCAAAATATCAAAATGAATATCAAAATATAGATGCGACACCT--TCTACTTCTGTA	60	
QY	23	SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr	42	
DB	61	TCCAATGATCTTAACAGATACCCCTTTTGGCAATGAGCAACAAATGCCGTACAAAATG	120	
QY	43	AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer	62	
DB	121	GATTAATGAATATTTAAATGCT-----GCGGAAATGCTAGT	162	
QY	63	ThrTyr---SerSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIle	81	
DB	163	GAATACCCCTGGTTCACTGAAGTACTTGTAGCGGACAAAGATGACGTAAGGCCCAATT	222	
QY	82	AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly	101	
DB	223	GATATAGTAGTAAATATCTACTATCAGGTTTAGGGTCCCATTTGTTGGGCGCATAGT	282	
QY	102	IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla	119	
DB	283	CTTTATATCACTTATTGATATCTGTGGCCCTTCAGGGGAAAAGATCAATGGGAATT	342	
QY	120	LeuMetValLeuValGluLeuIleLysSerIleAspGlnArgValArgGluAsn	139	
DB	343	TTTATGGAACAGTAGAAGACTCATTAATCAAAAATAGCAGATATCCAGGAATAA	402	
QY	140	AlaLeuArgGluLeuGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln	159	
DB	403	CGCCTTCGGATTAGAGGATTAGGTAAATATTACCAATTATATCTAACTCGCGTTGAA	462	
QY	160	AlaTrpLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla	178	
DB	463	GAATGGGAAGAAATCCAAATGGTTCAAGAGCCCTTACGAGATGTGCGAAATCGATTGAA	522	
QY	179	IleValAspAsnPheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle	198	
DB	523	ATCCTGGATAGTTTATTTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAATA	582	
QY	199	LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla	218	
DB	583	CCATTCCTTACTGTATGCAATGCGAGCCAACTTCATTTACTGTTATTAAGGACGCG	642	
QY	219	AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg	238	
DB	643	TCAATTTTGGAGAAGATGGGGATGGTCAACACTACTATTAAATACTATTATGATCGT	702	
QY	239	LeuGlnGlyIleLeuArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu	258	
DB	703	CAATGAAACTTACTGCGAGATATCTGATCACTGTGTAAAGTGGTATGAAACTGGTTTA	762	
QY	259	AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp	278	
DB	763	GCAAAATTAAGGACGCGCGCTAAACAAATGGGTGACTATAACCAATTCGCTAGAGAA	822	
QY	279	MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgTyr	298	
DB	823	ATGACACTGGCGGTTTATGATGTTTGTGATTTATTTCCCAATTTATGACACGCGACGTAC	882	
QY	299	ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr	318	

DB	883	CCAATGGAAACGAAAGCACAACCTAACAGGGAAGTATATACAGATCCACTGGCGCGGTA	942	
QY	319	GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe	338	
DB	943	AACGTGTCTTCAATGGTTC-----TGGTATGAC---AAAGCACCTTCTTCTTC	987	
QY	339	ThrAlaMetGluAsnAsnAlaArgArgProSerTyrThrThrTrpLeuAsnArgIle	358	
DB	988	GGAGTGATAGATCATCCGTTATTCGACCACCCCATGATTTGATTATATAACGGGACTC	1047	
QY	359	PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly	376	
DB	1048	ACAGTGTATACACAATCAAGAAGCATTTCTTCGCTCGCTATATAAGACAT---TGGGCT	1104	
QY	377	GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly	395	
DB	1105	GGTCATCAAAATAGCTACCATCGTGTAGTAGGGTAGTAATCTTCAACAATGATGTA	1164	
QY	396	LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer	415	
DB	1165	ACTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATATGATATTTACAAG	1224	
QY	416	IleGluSer-----LeuAlaArgIleTyrLeuGlyThrGluAlaAsn	430	
DB	1225	ACTCTATCAAAAGGATGCACTACTCTCTGATATTGTTTACCTCGTGTATACG-----	1275	
QY	431	AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle	449	
DB	1276	---TATATATTT-----TTTGGAAATGCCAAGTCGAGTTTTCATCGTAAACCAATTG	1326	
QY	450	AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle	469	
DB	1327	ATAATACCAAGAACAGCGTTAAAGTAT-----AATCCAGTTTCCAAGATATT	1374	
QY	470	LeuSer-----GluLeuProGlyLysAspLysProArgProAsn	482	
DB	1375	ATAGCGAGTCAAGAGATTCGGAATTAGAAATTACCTCCAGAAACTTCAGATCAACCAAT	1434	
QY	483	AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgSerSer	502	
DB	1435	TATGAGTCATATAGCCATAGATTATGTCAATCAACAGTATTTCCCGCACGGGTAACT	1494	
QY	503	SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn	522	
DB	1495	ACCGATTAGTACCT-----GTATTTCTTGGACACATCGAAGTCGAGATTAAAC	1545	
QY	523	AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn	542	
DB	1546	AATACATATATTCAGATAAAATCACTCAAAATTCGCGCGTTAAATGTTGG---GATAAT	1602	
QY	543	IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal	558	
DB	1603	TTACCGTTTGTTCAGTGGTAAAGGACCGAGACATACAGAGGGGATTTATTACAGTAT	1662	
QY	559	SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln	571	
DB	1663	AATAGAAGTACTGGTTCGTAGGACCTTATTTCTAGTCGATATGGCTAGCATAGAA	1722	
QY	572	ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla	591	
DB	1723	AAAGCAGGAAATATCGTGAAGACTGATATGCTACT-----GATGCA	1767	
QY	592	IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer	611	
DB	1768	GATATTGTTGTCATGTAAACGATGCTCAGATTACG-----ATGCCAAA	1812	
QY	612	SerGlyAspProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly	631	
DB	1813	ACATGAACCCAGGTGAGGATCTGACATCTAAACTTTTAAAGTTCGAGATCTATCACA	1872	
QY	632	IlePheThrProSerIleAsnProLeuIleArgTyrArg-----	644	
DB	1873	ACATTAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATAAATTTAGGTGAAGACCT	1932	

Qy	431	AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle	449
Db	1276	---TATATATTT---TTTGGAAATCCGAAGTCGAGTGTCTTTTTCATGGTAAACAATGTG	1326
Qy	450	AsnAsnValProGlySerLeuAtqTyrGluValProAlaAsnLeuProSerGlnThrIle	469
Db	1327	ATATATACCAGAAAGACGTTTAAAGTAT-----AATCAGGTTTCAAAAGATATT	1374
Qy	470	LeuSer-----GluLeuProGlyIleAspLysProArgProAsn	482
Db	1375	ATAGCGAGTACAAGAGATTCCGAATTAGAAATTACCTCCAGAAACTTCAGATCAACCAAAAT	1434
Qy	483	AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer	502
Db	1435	TATGAGTCATATAGCCATAGATTATGTCATATCACAAGTATTCGCCGCGGTAAATCTTGG--GATAAAT	1502
Qy	503	SerGlyGlyIleValSerLeuThrPheGlyTyrPalahisThrSerMetAspArgAsn	522
Db	1495	ACCGATTAGTACCT-----GTATTTCTTGGACACATCGAAGTCGAGATTTAAAC	1545
Qy	523	AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyGlyAsn	542
Db	1546	AATACAATATATTCAGATAAAATCACTCAAATTCGGCCGTTAAATCTTGG--GATAAAT	1602
Qy	543	IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal	558
Db	1603	TTACGTTTGTTCAGTGGTAAAGGACAGACATACGAGGGGATTTATTACAGTAT	1662
Qy	559	SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln	571
Db	1663	AATAGAAGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAA	1722
Qy	572	ArgGlnThrSerTyrArgIleAtqLeuArgTyrAlaCysLeuValThrHisGlyAspAla	591
Db	1723	AAACGAGGAAATATCGTTGAAGACTCAGATATGCTACT-----GATGCA	1767
Qy	592	IlePheValGluHisSerGlySerHisIleValSerPhePheAspCysSerAsnSer	611
Db	1768	GATATTGTATTGCATGTAAACGATGCTCAGATTCCAG-----ATGCCAAAA	1812
Qy	612	SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly	631
Db	1813	ACAATGAACCCAGGTGAGGATCTCACAATCTTAAACCTTTTAAAGTTGCAGATGCTATCACA	1872
Qy	632	IlePheThrProSerIleAsnProLeuIleArgTyrArg-----GAA	644
Db	1873	ACATTAATTTAGCAACAGATAGTTCCGTAGCATTTGAAACATAATTTAGGTGAAGACCCT	1932
Qy	645	---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn---	662
Db	1933	AATTCAACATTTATCTGGTGTATAGTTTACGTTTGACCGCAATTCGAATTTATCCCGAGTAGTAG	1992
Qy	663	ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle	681
Db	1993	ACATTAAGACCGGAACACAGATTTAGAAGCAGCGAAGAACAGTGAATGCTTGTTTACG	2052
Qy	682	Asn	682
Db	2053	AAT	2055

[illegible]


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QY 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
Db 1993 ACATATGAAGCGCAACAAGATTAGAAAGCAGCGCAAGAAAGCAGTGAATCCCTTGTTACG 2052
QY 682 Asn 682
Db 2053 AAT 2055

RESULT 5
US-11-021-115-5
; Sequence 5, Application US/11021115
; Publication No. US20050166284A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Andre
; APPLICANT: Flannagan, Ronald D.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Bill F.
; APPLICANT: Presnail, James K.
; APPLICANT: Rice, Janet A.
; APPLICANT: Wong, James F.
; APPLICANT: Yu, Cao-Guo
; TITLE OF INVENTION: Plant Activation of Insect Toxin
; FILE REFERENCE: 035718/285836
; CURRENT APPLICATION NUMBER: US/11/021,115
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 60/532,185
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-11-021-115-5

Alignment Scores:
Pred. No.: 3,04e-96 Length: 3621
Score: 948.00 Matches: 248
Percent Similarity: 50.9% Conservative: 119
Best Local Similarity: 34.4% Mismatches: 276
Query Match: 26.4% Indels: 78
DB: 10 Gaps: 25

US-10-782-096-2 (1-682) x US-11-021-115-5 (1-3621)
QY 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 4 AGTCCAAATATCAAAATGAATATGAATATATAGATGCGACACCT---TCTACTTCTGTA 60
QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 61 TCCATGATTCACAGATACCTTTTGGCAATGAGCCCAAAATGCGGTACAAATATG 120
QY 43 AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 121 GATTATGAAGATTATTAATAATGTCT-----GCGGAAATGCTAGT 162
QY 63 ThrTyr---SerSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 163 GAATACCCCTGGTTTCACTTACCTGAGTACTTGTAGCGGCAAGATGCGAGTAAAGCCGCAATT 222
QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 223 GATATAGTAGGTAATATCTACTAGGTTTGGGGTCCCATTTGTTGGGCCGAGTAGT 282
QY 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
Db 283 CTTTATACCTCACTTATTGATATTCTGTGGCCTTCAGGGGAAAGCAATGCGGAATT 342
QY 120 LeuMetValLeuValGluLeuLeuLysSerIleAspGlnArgValArgGluAsn 139
Db 343 TTTATGGAACAGTAGAAGAACTCATTAATCAAAAAATAGCAGAAATATGCAAGGAATAAA 402

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QY 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 403 GCGCTTCGGATTAGAAGATTAGTAATAATTACCAATTATATCTAATCGCTGAA 462
QY 160 AlaTrpLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
Db 463 GAATGGGAAGAAATCCAAATGGTTCAGAGCGCTTACGAGATGTGCGAAATCGATTTGAA 522
QY 179 IleValAspAsnPheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
Db 523 ATCTCTGGATAGTTATTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAGTA 582
QY 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
Db 583 CCATTCTCTTACTGTATATGCAATGGCAGCCAACTTCAATTACTTGTATTAAAGGACGG 642
QY 219 AspTyrPheGlyValGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
Db 643 TCAATTTTGGAGAAGAAATGGGGATGGTCAACAATCTATTATAAATACTATTATGATCGT 702
QY 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 703 CAAATGAAACTTACTGCAATATTTCTGATCACTGTGTAAAGTGGTATGAAACTGGTTTA 762
QY 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
Db 763 GCAAAATTAAGGAGCAGCAGCGCTAAACAATGGGTGACTATAACAATTCCTCGTAGAA 822
QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 823 ATGACACTGGCGGTTTGTAGTGTCTTGCATTATTCCCAAAATTATGACACACGACGTAC 882
QY 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
Db 883 CCATGGGAAACGAAAGCACTAAAGGGAAGTATATACAGATCCACTCGGCGCGGTA 942
QY 319 GlyValLeuGluSerGlyGlyArgThrTyrProTyrAsnProAsnAsnThrThrPhe 338
Db 943 AAGGTGCTCTCAATTTGGTTCC-----TGGTATGAC---AAACACCTCTCTTTC 987
QY 339 ThrAlaMetGluAsnAlaAlaArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
Db 988 GGAGTGATAGATCATCGTTTATTCGACCACCCCATGTATTTGGATTATATAACGGGACTC 1047
QY 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
Db 1048 ACAGTGATATACAAATCAAGAGCAATTTCTCCGCTCGCTATATAGACAT---TGGGCT 1104
QY 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
Db 1105 GGTCAATCAATAAGCTACCATCGTCTCAGTAGGGTAGTAACTTCAACAATGTATGTA 1164
QY 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
Db 1165 ACTAATCAAAATCTACACGACTAGTACCTTTGATTTTACGAATATGATATATACAAG 1224
QY 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyThrGluAlaAsn 430
Db 1225 ACTCTATCAAGGATGCACTACTCTCTGATATTTTACCTCCCTGGTTATACG----- 1275
QY 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
Db 1276 ---TATATATTT-----TTTGGATGCCAGNAGTCGAGTTTTCATGGTAAACCAATG 1326
QY 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
Db 1327 AATAATACCAGAAAGACGTTAAAGTAT-----AATCCAGTTTCCAAAGATATT 1374
QY 470 LeuSer-----GluLeuProGlyLysAspLysPheProArgProAsn 482
Db 1375 ATAGCGAGTACAGAGATTTCGGAATTAGAAATTACCTCCAGAAATCTCAGATCAACCAAT 1434

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QY 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgSerSer 502
Db 1435 TATGAGTCATATAGCATAGATTATGTCTATACACAGTATTTCCCGGACGGTAACT 1494
QY 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn 522
Db 1495 ACCGGATTAGTACTCT-----GTATTTCTTGACACATCGAAGTCAGATTAAAC 1545
QY 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValGlyGlyThrGlyGlyAsn 542
Db 1546 AATACAATATATTCAGATAAAATCACTCAAAATTCGCGCGTTAAATGTGG---GATAA 1602
QY 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValIleVal 558
Db 1603 TTACCGTTTGTCAGTGTAAAGGACGACATACAGGAGGGGATTTATACAGTAT 1662
QY 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
Db 1663 AATAGAGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCTAGCATTAGAA 1722
QY 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 1723 AAAGCAGGGAATATCGTTAAGACTGAGATATGCTACT-----GATGCA 1767
QY 592 IlePheValGluHisSerGlySerHisIleValSerPhePheAspCysSerAsnSer 611
Db 1768 GATATTGATTGCATGTAACCATGCTCAGATTCTAG-----ATGCCAAA 1812
QY 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 1813 ACAATGAACCCAGGTGAGGATCTGCACATCTAAACCTTTTAAAGTTGCAGATCTATCACA 1872
QY 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 1873 ACATTAAATTTAGCAACAGATAGTTGCTGACGATTTGAAACATAAATTTAGTGAAGACCCCT 1932
QY 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 1933 AATTCACAAATATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTAGATGAG 1992
QY 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
Db 1993 ACATATGAAGCGGAACAGATTTAGAACGACGCGAAGAACGAGTGAATTCCTTTAGC 2052
QY 682 Asn 682
Db 2053 AAT 2055
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RESULT 6

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US-10-032-717-27
; Sequence 27, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIORITY FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-10-032-717-27

Alignment Scores:
Pred. No.:      4,96e-96      Length:      4874
Score:          948.00      Matches:      248
Percent Similarity: 50.9%      Conservative: 119
Best Local Similarity: 34.4%      Mismatches: 276
Query Match:      26.4%      Indels:      78
DB:              5          Gaps:      25

US-10-782-096-2 (1-682) x US-10-032-717-27 (1-4874)
QY 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 734 AGTCCAAATAATCAAAATGAATATGAATATATAGATGCGACACCT---TCTACTTCTGTA 790
QY 23 SerAsnCysTyrProAtgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 791 TCCATGATTTCTAACAGATACCTTTTCGGAATGAGCCACAAATGCGCTACAAATATG 850
QY 43 AsnTyrLysGluTyrLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 851 GATTATAAGATATTATTAATAATGTCT-----GCGGAAATCGTAGT 892
QY 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 893 GAATACCCCTGGTTACCTTGAAGTACTTGTGTAGCGGACAAGATGCGAGCTAAGCCGCAATT 952
QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 953 GATATAGTAGTAAATTAATCTATCAGGTTAGGGTCCCATTTGTTGGGCCGCTAGTAGT 1012
QY 102 IleIleSerArgLeuIleGlyIleLeuTyrAlaGlyProAsp-----ProPheGluAla 119
Db 1013 CTTTATATACTCAACTTATTGATATTCTGTGGCTTCAGGGGAAAAGAGTCAATGGGAAATT 1072
QY 120 LeuMetValLeuValGluLeuIleLysSerIleAspGlnArgValArgGluAsn 139
Db 1073 TTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAATAGCAGAAATATGCAAGGAAATAA 1132
QY 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 1133 GCGCTTTCCGAATTAGAAGGATTAGGTAATTAATACCAATTATATCTAATCTACGCGTTGAA 1192
QY 160 AlaTyrLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
Db 1193 GAATGGGAAGAAAATCCAAATGGTTCAAGAGCCTTACGAGATGTGCGAAATCGAATTGAA 1252
QY 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
Db 1253 ATCTCGGATAGTTTATTTACGCAATATATGCCATCTTTTAGAGTGACAAAATTTGAAGTA 1312
QY 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
Db 1313 CAATTCCTTACTGTATATGCAATGCGACCAACCTTCAATTTACTGTATTAATAAGACGCG 1372
QY 219 AspTyrPheGlyValGlnTyrGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
Db 1373 TCAATTTTGGAGAAGATGGGATGGTCAACACTACTATTAATACTATTAATATGATCGT 1432
QY 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 1433 CAAATGAACCTTACTGCGAGAATATTCTGATCACTGTGTAAGTGTATGAAACCTGTTTA 1492
QY 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp 278
Db 1493 GCAAAATTAAGGCGCAGCGCTAAACAATGGGTTGACTATTAACCAATTTCCGTAGAGAA 1552
QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgTyr 298
Db 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgTyr 298
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1553	DB	ATGACAC	TCGCGGCTTTTAGATGTTGTTCATATTCCCAAATTATGACACACGACGCTAC	1617
299	QY	ProLeuAlaVal	ThrLeuLeuThrArgGluValTyrThrAspProValGlyPheThr	318
1613	DB	CCAATGGAA	CAAAAGCACAACTAAACAAGGGAAGTATATACAGATCCACTGGGCGCGGTA	1672
319	QY	GlyValLeu	GluSerGlyGlyArgThrTyrProTyrAsnProAsnAsnThrPhe	338
1673	DB	AACGTGTCT	CAATTGGGTTC-----TGGTATGAC---AAAGCACCTTCTTCTTC	1717
339	QY	ThrAlaMet	GluAsnAsnAlaArgArgProSerTyrThrTyrLeuAsnArgIle	358
1718	DB	GGAGTGAT	AGATATCATTCGGTTATTCGACCCCATGTTTGAATATATACGGGACTC	1777
359	QY	PheValTyr	Thr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTyrGly	376
1778	DB	ACAGTGAT	TATACAATCAAGAACGATTTCTCCGCTCGCTATATAAGACAT---TGGGCT	1834
377	QY	GlyHisThr	Leu-----ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly	395
1835	DB	GGTCATCAA	ATAAATAGCTACCATCGTGTGAGTGGGTAGTAACTCTCAACAAATGTATGGA	1894
396	QY	LysThrAsp	SerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer	415
1895	DB	ACTAATCAA	ATCTATACACAGCTACACAGCAGTACCTTTGATTTACGAATATATATTACAA	1954
416	QY	IleGluSer	-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn	430
1955	DB	ACTCTATCA	AAAGATGCGAGTACTCTTGATATGTTTACCCTGGTTATACG-----	2005
431	QY	AsnTyrIle	ThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle	449
2006	DB	---TATATAT	TTT-----TTTGGAAATGCGAAGTCGAGTTTTTTCATGGTAAACCAATTG	2056
450	QY	AsnAsnVal	ProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle	469
2057	DB	AATAATACC	AGAAAGACGTTAAAGTAT-----AATCCAGTTTCCAAAGATATT	2104
470	QY	LeuSer	-----GluLeuProGlyLysAspLysProArgProAsn	482
2105	DB	ATACGGAG	TACAAGAGATTCGGAATTAGAAATTACCTCAGAACTTCAGATCAACCAAT	2164
483	QY	AlaGlyAsp	PheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSer	502
2165	DB	TATGAGTCA	TATAGCCATAGATTATGTCATATCAAGATATCCCGCGACGGGTAACT	2224
503	QY	SerGlyGly	IleValSerLeuLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn	522
2225	DB	ACCGGATTA	GTAACCT-----GTATTTTCTTGGACACATCGAATGCGAGATTTAAAC	2275
523	QY	AsnArgLeu	GluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyGlyAsn	542
2276	DB	AATACAAT	ATATTCAGATAAATCACTCAATTCGCGCGGTAAATGTTGG---GATAAT	2332
543	QY	IleGlyPhe	ValIle-----ProGlyProThrGlyGlyAsnLeuLysVal	558
2333	DB	TTACCGTTT	GTGTTCCAGTGGTAAAGGACGAGCATACAGAGGGGATTTATTACAGTAT	2392
559	QY	SerAspSer	TrpHisSerLeuLysVal-----GlnAlaProGln	571
2393	DB	AATAGAAG	TACTGCTCTGTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATAGAA	2452
572	QY	ArgGlnThr	SerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla	591
2453	DB	ANACAGGGA	AAATATCGTGTAAAGTACTGAGATATGCTACT-----GATGCA	2497
592	QY	IlePheVal	GluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer	611
2498	DB	GATATTGT	ATGATGTAAACGATGCTCAGATTACG-----ATGCCAAA	2542
612	QY	SerGlyArg	ProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly	631
2543	DB	ACAATGAAC	CCAGGTGAGGATCTGACATCTAAACCTTTAAAGTTGCGAGATGCTATCACA	2602

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Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 2603 ACATTAAATTTAGCAACAGATAGTTCCTAGCATTTGAAACATATATTAGGTGAAGACCC 2662
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 2663 AATTCAACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCCGATAGATGAG 2722
Qy 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
Db 2723 ACATATGAAGCGGAACAAGATTTTAGAAGCAGCGAAGAACAGTGAATGCTTGTTTACG 2782
Qy 682 Asn 682
Db 2783 AAT 2785

RESULT 7
US-10-414-637-27
; Sequence 27, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Genomic DNA 1318-1
US-10-414-637-27

Alignment Scores:
Pred. No.: 4.96e-96 Length: 4874
Score: 948.00 Matches: 248
Percent Similarity: 50.9% Conservative: 119
Best Local Similarity: 34.4% Mismatches: 276
Query Match: 26.4% Indels: 78
DB: Gaps: 25

US-10-782-096-2 (1-682) x US-10-414-637-27 (1-4874)
Qy 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 734 AGTCCAAATTAATCAAAATGAATGAATGAATATATAGATGCGACACCT--TCTACTTCTGTGA 790
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 791 TCCAAATGATTCTAACAGATACCCCTTTTGGCAATAGCGCCAAACAAATCGCTACAAAATATG 850
Qy 43 AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 851 GATTATTAAGATTATTATTAATAATGTCT-----CCGGNAATGCTAGT 892
Qy 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81

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; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/263948
; CURRENT APPLICATION NUMBER: US/10/606,320
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-10-606-320-17

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Alignment Scores:

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Pred. No.: 4,96e-96 Length: 4874
Score: 948.00 Matches: 248
Percent Similarity: 50.9% Conservative: 119
Best Local Similarity: 34.4% Mismatches: 276
Query Match: 26.4% Indels: 78
DB: 7 Gaps: 25

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US-10-782-096-2 (1-682) x US-10-606-320-17 (1-4874)

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QY 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
DB 734 ACTCCAAATAATCAAAATGAATATGAATATAGATCGCACACT---TCCTACTCTGTA 790
QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
DB 791 TCCAATGATCTTAACAGATACCCCTTTTGGCAATGAGCCCAACAAATCGCGCTACAAATATG 850
QY 43 AsnTyrLysGluTyrLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
DB 851 GATTATAAGATATTTAAAAATGCT-----GCGGAAATGCTAGT 892
QY 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
DB 893 GAATACCTGGTTCACCTGAAGTACTTGTACGGCAAGATGCGAGTAAGGCCGCAATT 952
QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
DB 953 GATATAGTAGTAAATTAATCACTACAGTTTAGGGGTCCTCCATTTGTTGGCCGATAGT 1012
QY 102 IleIleSerArgLeuIleGlyIleLeuTyrAlaGlyProAsp-----ProPheGluAla 119
DB 1013 CTTTATACCTCAACTTATTGATATCTGTGGCTTCAGGGGAAAGAGCAATGGGAAATT 1072
QY 120 LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
DB 1073 TTTATGGAAACAGTAGAAGAACTATTATCAAAAATATGCAAAATATGCAAGGAATAA 1132
QY 140 AlaLeuArgGluLeuGluGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
DB 1133 GCGCTTTCCGAATTAGAGGATTAGTAATATTAATCACTAATATATCTAATCGCGCTTGA 1192
QY 160 AlaTyrLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
DB 1193 GAATGGGAAGAAATCCAAATGGTTCAAGAGCTTACGAGATGTCGCAAAATCGAATTGAA 1252
QY 179 IleValAspAsnPheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
DB 1253 ATCCCTGGATGATTTATTTACGCAATATATATGCCATCTTTTAGAGTGACAAATTTTGA 1312

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QY 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHleLeuIleLeuArgAspAla 218
DB 1313 CCATTCCTTACTGTATATGCAATGGCAACCTTCATTCTGTATGTTTAAAGACGG 1372
QY 219 AspTyrPheGlyAlaGlnTyrGlnLeuGlyAspAspGluIleArgAspAsnTyrIleAsp 238
DB 1373 TCAATTTTGGAGAAGATGGGATGGTCAACAACACTACTATTAACTATTATGATCCT 1432
QY 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
DB 1433 CAAATGAAACTTACTGCAAGATATCTGATCACTGTGTAAGTGGTATGAACTGGTTTA 1492
QY 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp 278
DB 1493 GCAAATTAAGGACGACGCGCTAAACAATGGGTTGACTATATACCAATTCGATAGAA 1552
QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgAspTyr 298
DB 1553 ATGACACTGGCGGTTTGTAGTGTGTTGCAATTTATCCCAATATATGACACACGCGTAC 1612
QY 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
DB 1613 CCAATGGAAACGAAAGCACTAACAAGGAAGTATATACAGATCCACTGGGCGGTA 1672
QY 319 GlyValLeuGluSerGlyGlyArgThrTyrProTyrPheAsnProAsnAsnThrThrPhe 338
DB 1673 AACGTGTCTTCAATTTGGTTCC-----TGGTATGAC---AAAGCACCTTCTTTC 1717
QY 339 ThrAlaMetGluAsnAsnAlaArgArgProSerTyrThrThrTyrLeuAsnArgIle 358
DB 1718 GGAGTGATAGAAATCATCGTTATTCGACCACCCCATGTATTGTATATATACGGGACTC 1777
QY 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTyrGly 376
DB 1778 ACAGTGTATACAACTCAAGAAGCATTTCTTCGCTCGCTATATAAGACAT---TGGGCT 1834
QY 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
DB 1835 GGTCAATCAATTAAGCTACCATCGTGTAGTGGGTAGTAAATCTTCAACAAATGTATGA 1894
QY 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
DB 1895 ACTAATCAAAATCTACAGCAGCTAGTACCTTTGATTTTACGAATATATGATATTTACA 1954
QY 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
DB 1955 ACTCTATCAAGAGATGAGTACTCTCTGTATATTGTTTACCTCGTGTATAGC----- 2005
QY 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
DB 2006 ---TATATATTT-----TTTGGATGCCAGAAGTCGAGTTTTTTCATGCTAAACCA 2056
QY 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
DB 2057 AATAATACCAAGAACGCTTAAAGTAT-----AATCCAGTTTCCAAAGATATT 2104
QY 470 LeuSer-----GluLeuProGlyLysAspLysPheProArgProAsn 482
DB 2105 ATAGCGAGTACAGAGATTCGGATTAAGATTACCTCCAGAACTTCAGATCAACCAAT 2164
QY 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgSerSer 502
DB 2165 TATGAGTCATATAGCCATAGATTATGTATCATATCACAAGTATTTCGCGCGGTAACACT 2224
QY 503 SerGlyGlyIleValSerLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn 522
DB 2225 ACCGATTAGTACCT-----GTATTTCTTGGACACATCGAAGTGCAGATTAAAC 2275
QY 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyGlyAsn 542
DB 2276 AATCAATATATTCAGATAAATCACTCAATTCGCGCGGTTAAATGTGG---GATAAT 2332
QY 543 IleGlyPheValIle-----ProGlyProThrGlyAsnLeuValLysVal 558

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Db 2333 TTACGGTTTGTTCAGTGTAAAGGACGACATACAGGAGGGGATTTATACAGTAT 2392
Qy 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
Db 2393 AATGAAGTACTGGTCTGTAGAAACCTTATTTCTAGCTCGATATGGCCATAGCA 2452
Qy 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 2453 AAAGCAGGAATAATTCGTAGATAGCTGAGATATGCTACT-----GATGCA 2497
Qy 592 IlePheValGluHisSerGlySerHisIleValSerPheAspCysSerAsnSer 611
Db 2498 GATATTGATTGCAATGAACGATGCTCAGATTTCAG-----ATGCCAATA 2542
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 2543 ACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCAGATGCTATCACA 2602
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 2603 ACATTAAATTTAGCAACAGATAGTTGCGTAGCATTTGAAACATAAATTTAGGTGAAGACCT 2662
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 2663 AATTCAACATATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTAGATGAG 2722
Qy 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
Db 2723 ACATATGAAGCGGAACAAGATTTAGAAGCAGCGGAAGAAAGCAGTGAATGCCCTTGTTTACG 2782
Qy 682 Asn 682
Db 2783 AAT 2785

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RESULT 9

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US-10-746-914-17
; Sequence 17, Application US/10746914
; Publication No. US20040210963A1
; GENERAL INFORMATION:
; APPLICANT: Albert L. Lu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/268350
; CURRENT APPLICATION NUMBER: US/10/746,914
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-10-746-914-17

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Alignment Scores:

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Pred. No.: 4,96e-96 Length: 4874
Score: 948.00 Matches: 248
Percent Similarity: 50.9% Conservative: 119
Best Local Similarity: 34.4% Mismatches: 276
Query Match: 26.4% Indels: 78
DB: 8 Gaps: 25

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US-10-782-096-2 (1-682) x US-10-746-914-17 (1-4874)

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Qy 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 734 AGTCAAATAATCAAAATGAATATGAATATAGATGCGACACCT---TCTACTTCTGTGA 790
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 791 TCCAATGATTCTAACAGATACCCCTTTGCGAATGAGCCCAACAAATGCGCTACAAATATG 850
Qy 43 AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 851 GATTATAAGATTAATTTAAAAATGTCT-----GCGGAAATGCTAGT 892
Qy 63 ThrTyr---SerSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 893 GAATACCCCTGGTTACCTGGAAGTACTTGTAGCGGCAAGATGCGAGCTAAGGCCCGCAATT 952
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 953 GATATAGTAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1012
Qy 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
Db 1013 CTTTATACTCAACTTATTGATATCTGTGGCCTTCAGGGGAAAGAGTCAATGGGAAATT 1072
Qy 120 LeuMetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
Db 1073 TTTATGGAAACAGTAGAAGAACTCATTAATCAAAAATAGCAGAAATATGCAAGGAATAA 1132
Qy 140 AlaLeuArgGluLeuGluGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 1133 CGGCTTTCCGGAATTAGAAGGATAGGTAAATTAATTAATTAATTAATTAATTAATTAAT 1192
Qy 160 AlaTrpLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
Db 1193 GAATGGGAAGAAATCCAAATGGTTCAGAGCCTTACGAGATGTCGGAATTCGATTGAA 1252
Qy 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
Db 1253 ATCTGGATAGTTTATTACGCAATATATATGCAATCTTTTAGAGTGACAAATTTGAAGTA 1312
Qy 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
Db 1313 CCATTCCTTACTGTATATGCAATGGCAGCCAACTTCAATTTACTTGTATTAAGGACGCG 1372
Qy 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
Db 1373 TCAATTTTGGAGAAGATGGGATGGTCAACAACACTACTATTATAAATACTATTATGATCGT 1432
Qy 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 1433 CAATATGAACCTTACTGCGAATAATTTCTGATCAGTGTAAAGTGGTATGAACCTGGTTA 1492
Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
Db 1493 GCAAAATTAAGGCGCAGCGCTAAACAATGGGTGACTATAACCAATTCGCTAGAGAA 1552
Qy 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 1553 ATGACACTGGCGGTTTATAGATGTTGTCATTATTCCTCAAAATTAATGACACACGCGTAC 1612
Qy 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
Db 1613 CCAATGGAAACGAAAGCAACTAACAGGAAGTATATACAGATCCCATCGGCGCGGTA 1672
Qy 319 GlyValLeuGluSerGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338
Db 1673 AACGTGCTTCAATTGGTTCC-----TGGTATGAC---AAAGCACCTTCTTTC 1717
Qy 339 ThrAlaMetGluAsnAsnAlaArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
Db 1718 GGAGTGATAGAAATCATCGTTATTTCGACACCCCATCGATTATTTGATTATATTAACGGGCTC 1777

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QY 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
Db 1778 ACAGGTATACAAATCAAGAAGCATTTCTTCGCTCGCTATATAGACAT--TGCGCT 1834
QY 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
Db 1835 GGTCAATCAATAGCTACCATCGTGCAGTAGGGGTAGTAATCTTCAACAATGTATGA 1894
QY 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
Db 1895 ACTAATCAAAATCTACACGACTAGTACTTGTGATTTTACGAATATGATATTTACAAG 1954
QY 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
Db 1955 ACTTATCAAAAGATCAGTACTCTTGTATATTGTTTACCCTGGTTATACG----- 2005
QY 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
Db 2006 ---TATATATTT-----TTTGGATGCCAGAGTCGAGTTTTCATGTTAAACCAATG 2056
QY 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
Db 2057 AATAATACCAGAAAGACGTTAAAGTAT-----ATCCAGTTTCCAAAGATATT 2104
QY 470 LeuSer-----GluLeuProGlyLysAspLysProArgProAsn 482
Db 2105 ATAGCGAGTACAGAGATTCGGAATTAGAATTAACCTCCAGAAATCTTCAGATCAACCAAT 2164
QY 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgSerSer 502
Db 2165 TATGAGTCATATAGCCATAGATTATGTCATATACAAAGTATTCCCGCGCAGCGGTAACT 2224
QY 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn 522
Db 2225 ACCGGATTAGTACCT-----GTATTTCTTGGACACATCGAAGTCAGATTAAAC 2275
QY 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyAsn 542
Db 2276 AATAACAATATATTCAGATAAAATCACTCAAAATCCCGCGGTTAAATGTTGG---GATNAT 2332
QY 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal 558
Db 2333 TTACCGTTTGTTCACGTGTAAAGACCGAGGACATACAGGAGGGGATTTATTACAGTAT 2392
QY 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
Db 2393 ATAGAAGTACTGGTTCTGTAGGAACCTTATTCTAGCTCGATATGCGCTAGCATTAGAA 2452
QY 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 2453 AAAGCAGGGAATATCGTGTAGACTGAGATATGCTACT-----GATGCA 2497
QY 592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
Db 2498 GATATTGTATTGATGTAACCGATGCTCAGATTTCAG-----ATGCCAAA 2542
QY 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 2543 ACATGACCAGAGTGTAGATCTGACATCTAAACCTTTTAAAGTTCCAGATGCTATCACA 2602
QY 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 2603 ACATTAAATTTAGCAACAGATAGTTCCGTAGCATTTGAAACATAATTTAGTGAAGACCCT 2662
QY 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 2663 AATTCAACATTAATCTCGTATAGTTTACGTTGACCGGAATCGAATTCATCCAGTAGATGAG 2722
QY 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnValAsnAspLeuPheIle 681
Db 2723 ACATATGAAGCGGAACAGATTTAGAAAGCAGCGCAAGAAAGCAGTGAATGCCTGTTTACG 2782
QY 682 Asn 682
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Db 2783 AAT 2785
RESULT 10
US-10-089-678-2
; Sequence 2, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(3501)
; OTHER INFORMATION:
US-10-089-678-2

Alignment Scores:
Pred. No.: 2,07e-95 Length: 3504
Score: 940.50 Matches: 256
Percent Similarity: 51.8% Conservative: 111
Best Local Similarity: 36.1% Mismatches: 288
Query Match: 26.1% Indels: 56
DB: Gaps: 23

US-10-782-096-2 (1-682) x US-10-089-678-2 (1-3504)
QY 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 4 AGTCCAAATAATCAAAATGAATATGAATTCAGATGCT---TCATCATCTACTTCTGTGA 60
QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 61 TCGGATTAATCTGTAGATACCTTTAGCAACGATCAACGACCATACAAACATG 120
QY 43 AsnTyrLysGluTyrLeuAsnMetCysAsp---SerAsnThrGlnPheIleGlyAspIle 61
Db 121 AACTATAAAGATTATCTGAGAATGCTGAGGAGAGAAATCTCGAATTTATTGGAAATCCG 180
QY 62 SerThrTyrSerSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 181 GAGACGTTTATTAGT-----TCATCTACGGTTCAAACCTGGAAT 219
QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 220 GGCATTGTGTCAAGTACTGGGGCTTTAGGGTTCCATTTGCTGGACAGATAGTAGT 279
QY 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyPro-----AspProPheGluAla 119
Db 280 TTTTATAGTTTCATTGTCGTCATTTATGCGCATCAAGTACCGTGTAGTGTATGGGAAATG 339
QY 120 LeuMetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
Db 340 ATTATGAAACAAGTGGAGATCTAATTTGATCAAAAATAAACAGATTTCTCTAAGGAACA 399
QY 140 AlaLeuArgGluLeuGluGlnGlnGlyIleMetArgLeuThrGlnThrArgLeuGln 159
Db 400 GCGCTTCAGGACTACAGAGATTAGGAGATGGCTTAGAGCTATATCAGAAATCACAATAG 459
QY 160 AlaTrpLeuValAsnLysAsnAspAsnArgAla---LeuValThrGlnTyrAla 178
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Db 190 AGTCCAAATATCAAAATGAATATGAAATCTAGATGCT---TCATCATCTACTTCTGTA 246
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 247 TCCGATAATTCTGTAGATACCTTTAGCAACGATCAAAACGACACATTAACAAACATG 306
Qy 43 AsnTyrLysGluTrpLeuAsnMetCysAsp---SerAsnThrGlnPheIleGlyAspIle 61
Db 307 AACTATAAGATATCTGAGAATGCTGAGGGAGAGAATCTCGAATATTATTGGAAATCG 366
Qy 62 SerThrTyrSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 367 GAGAGCTTATAGT-----TCATCTACCGTTCAAACTGGAAT 405
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 406 GCGATTGTTGGTCAAGTACTGGGGCTTTAGGGTTCCATTGCTGGACAGATAGT 465
Qy 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyPro-----AspProPheGluAla 119
Db 466 TTTTATAGTTTCATTTGTCGGTCAATATATGGCCATCAAGTACCGTGAGTGTATGGGAATG 525
Qy 120 LeuMetValLeuValGluLeuIleLysSerIleAspGlnArgValArgGluAsn 139
Db 526 ATTATGAACAAGATGGAAGATCTAATGTATCAAAATAACAGATTCGTGAAGGAACA 585
Qy 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 586 GCGCTTGCAAGTACAGGATTAGGAGATGCGTTAGACGTATATACAGAAATCACTTAAG 645
Qy 160 AlaTrpLeuValAsnLysAsnAspAsnArgAla---LeuValThrGlnTyrAla 178
Db 646 AATTGCGTGGAAATCGTAATGATCAAGAGCTAGAAAGTGTGTGTGACCCCAATATATA 705
Qy 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
Db 706 GCTTTAGAGCTTGATTTGTTGCTAAAATCCCATCTTTTGCATATCTGGACAGGAAGTA 765
Qy 199 LeuLeuLeuProValTyrAlaGlnAlaAsnLeuHleLeuLeuArgAspAla 218
Db 766 CCATTTATATCATGTATGCACAGCAGCGAATTTACATTTGCTATTATTACAGATGCT 825
Qy 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
Db 826 TCCATTTTGGACAGAGTGGCGATTACACCAGCAGAGAAATTCACCATTTTATGATGCT 885
Qy 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 886 CAGGTGACACGTACCGCCCAATACTCGGAATTTATGTGTAAGTGTGTAACACTCGCTTA 945
Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
Db 946 GATAAATTAAGAGGTACGATGCTGCAAGTGGCTGAAGTATCAACAATTCGCAAGAGAA 1005
Qy 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 1006 ATGACATTACTGTTATAGATTAGTGGTATTATTTCCAAACTATGACACACGTACGTAT 1065
Qy 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
Db 1066 CCNATCGAAACAAACCGCCCAACTTACCGGGAAGTGTATACAGATCCCAATATTAAC 1125
Qy 319 GlyValLeuGluSerGlyGlyArgThrTyrProTyrTyrAsnProAsnAsnThrThrPhe 338
Db 1126 AGAGAA---ACAAGTGGTGATTTGTAGGCGTTGTCATCTTAACAGATGATATTTCTTT 1182
Qy 339 ThrAlaMetGluAsnAlaAlaArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
Db 1183 TCAGAAAGTCGAAGCGTGAATTCGTTCCACCACACCTATTATGATATACTCAGTGAATA 1242
Qy 359 PheValTyrThrArgThrLeuGly-----AsnMetSerAspValArgAsnIleTrp 375
Db 1243 GAAATTTTATCAACAAGACGCGGCTTCCCTTGAATAATACGGAATACCTTGAATATTGG 1302

RESULT 12

US-10-032-717-5

; Sequence 5, Application US/10032717

; Publication No. US20020151709A1

Qy 376 GlyGlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPhe 394
Db 1303 GTAGACATCTTATAAAATATAGAAATGCTCATCAGCATTAGAACGTAATATAC 1362
Qy 395 GlyLysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPhe 414
Db 1363 GGT---ACGATTACTTAAACAAATCAAGTATATGATTTAGCAAAATAGGATATCTTT 1419
Qy 415 SerIleGluSerLeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsnAsnTyrIleThr 434
Db 1420 CAGGTTCCGATCATTA-----GGGGCGGATTAGCTAATTTACTACGCA 1461
Qy 435 SerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnIleAsnAsnValProGly 454
Db 1462 CAGGTATATGAGATTCGCTAGCTAGTTTACACTGCTTGACAGAATAACAGATCAGGA 1521
Qy 455 SerLeu-----ArgTyrGluValProAlaAsn-----LeuProSer 466
Db 1522 TCAGTTGGAGGTTTACGTACTCAAAACCAACATACACTATGCAAGTATGTACACAAAT 1581
Qy 467 GlnThrIleLeuSerGluLeuProGlyLysAspLysProArgProAsnAlaGlyAspPhe 486
Db 1582 TACAATCAGATTGATGAATCCCTCCAGAGATGAGCCACTTAGTAGAGGG-----TAT 1635
Qy 487 SerHisArgLeuSerTyrIleSer-----AsnPheAspAlaArgArgSerSerGly 504
Db 1636 AGCCATAGATTATCTCATATCACCTCTATTCTTTTCTAAGAAATGCTAGTAGTCTGCT 1695
Qy 505 GlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsnAsnArg 524
Db 1696 AGATATGCAATCTCCCTGTTATTTCTGGACACATCGGAGTGGCGATGTTTCAAAATAC 1755
Qy 525 LeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrp-----GlyGly 541
Db 1756 GTTATTTCAGATTAATTTACTCAGATACCATGTTGTAAAGGCACATCTTAGTTTCAGGT 1815
Qy 542 AsnIleGlyPheValIleProGlyProThrGlyGlyAsnLeuValLysValSerAspSer 561
Db 1816 ACTACTGTTATTAAAGGCTCTGATTTACAGAGGCAATATCTTTAAAGAACAAAGTAGT 1875
Qy 562 -----TrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArg 577
Db 1876 GGTCTGTTAGCTTATACATGCTCTCTGTAAAAATCACCATTATCAAA---AGATATCGT 1932
Qy 578 IleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHisSer 597
Db 1933 GCAGAAATACGTTATGCTTCT-----ACTACTAACTTACGACTTTTGTAAACAATTTCT 1986
Qy 598 GlySerSerHisIleValSerPheAspCysSerAsnSerSerGlyArgProSerAsn 617
Db 1987 GGAAC-TCGCATTATCTC-----TATAAATGTT--AATAAAACCATGAATAAAGGGAT 2037
Qy 618 ThrLeuLeuGluSerAspPheArgTyrIleAspValProGlyIlePheThr---ProSer 636
Db 2038 GATTTAACATTTAATACATTTGACTTAGCAACTATTGTTACTGCTTTTCACATTTTCAAT 2097
Qy 637 IleAsnProLeuIleArgTyrArgThrGlnSerPhe-----GlyThrHisAlaIle 653
Db 2098 TACTCGGATAGCTTAAACGTTAGTGCAGATTCTTTTGTCTTACGAGGAGAAAGTATATGTA 2157
Qy 654 AspLysPheGluPheIleProLeuAsn---ThrPhe---ProAsnGlnSerLeuGluLys 671
Db 2158 GATAAGTTGGAATCTTATTCGGTAAATGCAACATTTGAAGCAGAGAACACCTAGATGTG 2217
Qy 672 ArgGluGlnGluValAsnAspLeuPhe 680
Db 2218 GCAAGAAAGCAGATAAATGGCTTGT 2244

QY 523 AenArgLeuGluProAspLysIleThrGlnIleAspAlaValIleGlyTrpGlyGlyAen 542
DB 1546 AATCAATATATATTCAGATAAATCACTCAATTCGCGCGTTAAATGTTGG---GATAT 1602
QY 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAenLeuValIleVal 558
DB 1603 TTACCGTTTGTTCAGTGTAAAGGACCAAGGACATACAGGAGGATTTTATACAGTAT 1662
QY 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
DB 1663 AATAGAAGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATAGAA 1722
QY 572 ArgGlnThrSerTrpArgIleArgLeuArgTrpAlaCysLeuValThrHisGlyAspAla 591
DB 1723 AAAGCAGGGAATATATCGTGTAGACTGAGATGCTACT-----GATGCA 1767
QY 592 IlePheValGluHisSerGlySerHisIleValSerPhePheAspCysSerAenSer 611
DB 1768 GATATGTTATTCGATGTAACCATGCTCAGATTCTAG-----ATGCCAAMA 1812
QY 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTrpIleAspValProGly 631
DB 1813 ACAATGAACCCAGGTGAGGATCTGACATCTAAACCTTTTAAAGTTCAGATGCTATCACA 1872
QY 632 IlePheThrProSerIleAsnProIleAsnProIleArgTrpArg-----644
DB 1873 ACATTAATTTAGCAACAGATAGTTCGCTAGCATGTAACATAAATTTAGGTGAAGACCT 1932
QY 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAen 662
DB 1933 AATTCAACATTAATCTGGTATAGTTTACGTGTGACCAATCGAATTCATCCAGTAGAT 1989

RESULT 13

US-10-414-637-5
; Sequence 5, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Peng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637

; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5

; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2001)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1

US-10-414-637-5

Alignment Scores:

Pred. No.: 3,72e-94 Length: 2003
Score: 926.00 Matches: 239
Percent Similarity: 50.8% Conservative: 116
Best Local Similarity: 34.2% Mismatches: 268
Query Match: 25.7% Indels: 76

DB: 6 Gaps: 23
US-10-782-096-2 (1-682) x US-10-414-637-5 (1-2003)
QY 3 SerTrpLysAsnLysAsnGlyTrpGluMetLeuAspAlaLeuArgIleAenSerAenMet 22
DB 4 AGTCCAAATAATCAAAATGAATATGAATTTATAGATGCGACACCT---TCTACTTCTGTA 60
QY 23 SerAsnCy8TyProArgTrpProLeuAlaLysAspProGlnMetThrMetArgAenThr 42
DB 61 TCCATGATTCTTAACAGATACCTTTTGGATGAGCCAAACAATGCGCTACAAAATATG 120
QY 43 AenTrpLysGluTrpLeuAenMetCysAspSerAenThrGlnPheIleGlyAspIleSer 62
DB 121 GATTATAAGATTATTTAAAAATGTCT-----GCGGAAATGCTAGT 162
QY 63 ThrTrp---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
DB 163 GAATACCTCGTGTTCACCTGAAGTACTTGTAGCGGACAGATGCGAGCTAAGCGCGCAAT 222
QY 82 AenSerValGlyThrIleLeuSerAenLeuGlyValProLeuAlaSerGlnSerPheGly 101
DB 223 GATATAGTAGTAAATTAATTAATCAGTTTGGGGTCCCATTTGTTGGGCGGATAGTAGT 282
QY 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
DB 283 CTTTATCTCAACTTATTGATATTCTGTGGCCTTCAGGGGAAAGAGTCAATGGGAAT 342
QY 120 LeuMetValLeuValGluLeuIleLysSerIleAspGlnArgValArgGluAen 139
DB 343 TTTATGGAACCAAGTAGAAGAACTCAATTAATCAAAAATAGCAGAAATATGCAAGGAATAA 402
QY 140 AlaLeuArgGluLeuGlyLeuGlnGlyIleMetArgLeuTrpGlnThrArgLeuGln 159
DB 403 GCGCTTCGGAATTAGAAGGATTAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 462
QY 160 AlaTrpLeuValAsnLysAsnAspAenArg---ArgAlaLeuValThrGlnTrpAla 178
DB 463 GAATGGGAAGAAATCCAAATGGTTACGAGCGCTTACGAGATGTCGAAATCGATTTGAA 522
QY 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
DB 523 ATCTCGATAGTATTATTCACCAATATATATGATGATGATGATGATGATGATGATGATGAT 582
QY 199 LeuLeuProValTrpAlaGlnAlaAlaAenLeuHisLeuIleLeuLeuArgAspAla 218
DB 583 CCATTCCTTACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 642
QY 219 AspTrpPheGlyAlaGlnTrpGlnLeuGlyAspGluIleArgAspAenTrpIleArg 238
DB 643 TCAATTTTGGAGAAAGATGGGATGGTCAACCACTACTATTATAAATCTATTATGATCGT 702
QY 239 LeuGlnGlyLeuIleArgGluTrpLysAspHisCysIleThrPheTrpAenGlnGlyLeu 258
DB 703 CAAATGAACCTTACTGCAAGATATTTCTGATCCTGTAAGTGTAAAGTGTAAAGTGTAAAG 762
QY 259 AenGlnPheAenArgSerAsnAlaGlnAspTrpValSerPheAenArgPheArgThrArg 278
DB 763 GCMAAATTAAGGACGAGCGCTAAACAAATGGGTTGACTATAACCAATTCCTGAGAGAA 822
QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAenTrpAspProArgTrp 298
DB 823 ATGACACTGGCGGTTTTAGATGTTTGTGATTTATTTCCCAATTTATGACACACGACGTAC 882
QY 299 ProLeuAlaValLysThrGluLeuThrArgGluValTrpThrAspProValGlyPheThr 318
DB 883 CCAATGGAAACGAAAGCAACTAACAGGGAAGTATATACAGATCCACTGGGCGCGTA 942
QY 319 GlyValLeuGluSerGlyArgThrTrpProTrpTrpAenProAenAenThrThrPhe 338
DB 943 AACGTGCTTCAATTTGGTTCC-----TGGTATGAC---AAAGACCTCTCTTTC 987
QY 339 ThrAlaMetGluAenAsnAlaArgArgProSerTrpThrThrTrpLeuAenArgIle 358

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Db 988 GGAGTGATAGATATCCGTTATTCGACCACCCCATGTATTGGATTATATACGGGACTC 1047
Qy 359 PheValThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
Db 1048 ACAGTGTATACAAATCAAGAAGCATTTCTCCGTCGCTATATAGACAT---TGGGCT 1104
Qy 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
Db 1105 GGTCAATCAATNAGCTACCATCGTGTACGAGGGTAGTAATCTTCAACAATATGTATGA 1164
Qy 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
Db 1165 ACTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATATGATATTTACAAG 1224
Qy 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
Db 1225 ACTCTATCAAGAGATCGCAGTACTCTTGATATGTTTACCCCTGGTTATACG----- 1275
Qy 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
Db 1276 ---TATATATTT-----TTTGGATGCGAAGTCGAGTTTTCATGTTAAACCAATGTG 1326
Qy 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
Db 1327 AATAATACCAAGAAGACGTTAAAGTAT-----AATCCAGTTTCCAAAGATATT 1374
Qy 470 LeuSer-----GluLeuProGlyLysAspLysProArgProAsn 482
Db 1375 ATAGCGAGTACAAGAGATTCCGGAATTTAGAAATTTACCTCCAGAAATCTCAGATCAACCAAT 1434
Qy 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSer 502
Db 1435 TATGAGTCATATAGCATTAGATATATGTCATATCACAAGTATTTCCCGCAGCGGTAACT 1494
Qy 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn 522
Db 1495 ACCGGATTAGTACCT-----GTATTTTCTGGACATCGAAGTCAGATTTTAAAC 1545
Qy 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn 542
Db 1546 AATACAATATATTCAGATAAAATCACTCAAATTCGCGCGTGTAAATGTTGG---GATAAT 1602
Qy 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal 558
Db 1603 TTACCGTTTGTCCAGTGTAAAGACGACGACATACAGGAGGGGATTTATTACAGTAT 1662
Qy 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
Db 1663 AATAGAAGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCTAGCATTAGAA 1722
Qy 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 1723 AAAGCAGGGAATATATCGTTAAGACTTGATATGCTACT-----GATGCA 1767
Qy 592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
Db 1768 GATATTGATTGCATGTAACGATGCTCAGATTTCAG-----ATGCCAAA 1812
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 1813 ACAATGAACCCAGGTGAGGATCTGACATCTAAACTTTTAAAGTTGCAGATGCTATACA 1872
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 1873 ACATTAATAATTAGCAACACATAGTTTCGCTAGCATTTGMAAATAATTTAGGTGAAGACCT 1932
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn 662
Db 1933 AATTCAACATATCTGGTATAGTTTACGTTGACCGAATTCGAATTCATCCAGTAGAT 1989
RESULT 14
US-10-032-717-9
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; Sequence 9, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1e1 Proteins With
; FILE OF INVENTION: Pesticidal Activity Against Coleopterans
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; OTHER INFORMATION: Maize optimized Cry12I8-1
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: mol1218-1
US-10-032-717-9

Alignment Scores:
Pred. No.: 3,74e-94 Length: 2010
Score: 526.00 Matches: 239
Percent Similarity: 50.8% Conservative: 116
Best Local Similarity: 34.2% Mismatches: 268
Query Match: 25.7% Indels: 76
DB: 5 Gaps: 23

US-10-782-096-2 (1-682) x US-10-032-717-9 (1-2010)
Qy 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 4 TCCCCCAACAACAGACGAGTACGAGATCATCGAGCGCACCCCC---TCCACCTCCGTG 60
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 61 TCCAAACGACTCCAACCGCTACCCCTTCGCCAACGAGCCACCAACGCGCTCCAGAACATG 120
Qy 43 AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 121 GACTACAAGGACTACCTCAAGATGTCC-----GCCGGCAACGCCCTCC 162
Qy 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 163 GAGTACCCCGGCTCCCGAGGTGCTCGTGTCCGCCAGAGCGCGCCCAAGCGCCCATC 222
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 223 GACATCGTGGGCAAGCTCTCTCCGGCTCGCGGTGCGCTTCGTGGGCGCCCATCGTGTCC 282
Qy 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
Db 283 CTCTACACCCAGCTCATGACATCTCTGGGCCCTCCCGCGAGAAAGTCCAGTGGGAATC 342
Qy 120 LeuMetValLeuValGluLeuIleLysSerIleLysSerIleAspGlnArgValArgGluAsn 139
Db 343 TTCATGGAGCAGGTGGAGAGCTCATCAACAGAAAGATCGCGAGTACGCCCGCAACAAG 402
Qy 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 403 GCCCTCTCCGAGCTGGAGGGCTTCGGCAACAACATACCAAGCTCTACCTCACCCTCGGAG 462
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QY 160 AlaTrpLeuValIleAsnLysAsnAspAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
DB 463 GAGTGGAGAGAACCCCAAGGCTCCCGCGCTCCGCGACGTGCGCAACCGCTTCGAG 522
QY 179 IleValAspAsnPheGluLysAsnMetProLysPheLysGluArgAsnGluIle 198
DB 523 ATCTCGACTCCCTCTACCCAGTACATGCTCTCTCGCGTGACCACTTCGAGGTG 582
QY 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuLeuLeuLeuArgAspAla 218
DB 583 CCCTTCTCAGCGTGACGCGCATGCGCGCAACTCCACTCTCTCTCAAGGACGCC 642
QY 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
DB 643 TCATCTTCGCGAGAGTGGGCTGCTCCACACCATCAACACTACTACGACCGC 702
QY 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
DB 703 CAGATGAAGTCAACCGCGAGTACTCCGACCACTGGGTGAAGTGTATGAGCCGCTC 762
QY 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp 278
DB 763 GCAAGCTCAAGGGACCTCCGCAAGCAGTGGGTGACTACACCACTTCGCGCGAG 822
QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
DB 823 ATGACCTCGCGTGCTGACGTGGTGGCCCTCTTCCCACTTACGACACCGCGCACTAC 882
QY 299 ProLeuAlaValIleThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
DB 883 CCATGGAGACCAAGCCAGCTCACCGCGAGGTGTAACCGACCGCTCGCGCGCGTG 942
QY 319 GlyValLeuGluSerGlyArgThrTyrProTyrAsnProAsnAsnThrThrPhe 338
DB 943 AAGGTGCTCTCATCGCTCT-----TGTACGAC---AAGGCCCCCAAGCTTC 987
QY 339 ThrAlaMetGluAsnAlaAlaArgArgProSerTyrThrTrpLeuAsnArgIle 358
DB 988 GCGGTGATGAGTCTCTCGTGATCGCGCGCGCAGTTCGACTACATCATCCGCGCTC 1047
QY 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
DB 1048 ACCGTGTATACCAAGTCCCGCTCCATCTCTCCGCGCGCTACATCGCCAC---TGGGCC 1104
QY 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
DB 1105 GGCACACAGATCTCTACACCGCTGTCGCGCTCAACTCCAGCAGATGTACGCG 1164
QY 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
DB 1165 ACCAACCAAGAACTCCACTCCACCTCCACTTCGACTTCACCACTTACGACATCTACAAG 1224
QY 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
DB 1225 ACCCTCTCAAGGACCGCGTGCTCTCGACATCGTGTACCGCGGTACACC----- 1275
QY 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
DB 1276 ---TACATCTC-----TTCGCGATCGCGAGGTGAGTCTTCATGTTGAACGAGCTC 1326
QY 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
DB 1327 AACAAACCCGCAAGACCTCAATAC-----AACCCGCTGTCCAAGGACATC 1374
QY 470 LeuSer-----GluLeuProGlyLysAspLysProArgProAsn 482
DB 1375 ATCGCTTCCACCGGACTCCGAGCTCCGAGCTCCCGCGAGACCTCCGACCGCCCAAC 1434
QY 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgSerSer 502
DB 1435 TACGAGTCTCTCTCCACCGCTCTGCGACATCATCTCCATCCCGCGCACCGGCAACACC 1494
QY 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn 522

DB 1495 ACCGGCTCGTCCG-----GTGTTCTCTCGACCAACCGCTCTCGACACCTCAAC 1545
QY 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValIleGlyTrpGlyGlyAsn 542
DB 1546 AACACCATCTACTCCGCAAGATCACCAAGATCCCGCGCTGAAGTGTGG---GACAAC 1602
QY 543 IleGlyPheValIle-----ProGlyProThrGlyAsnLeuValVal 558
DB 1603 CTCCTCTCGTCCGCTGGTGAAGGCGCCCGGCACACCGCGCGCAGCTCTCTCCAGTAC 1662
QY 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
DB 1663 AACCGCTCCACCGCTCCGTTGGGCACTCTCTCTCGCCGCTACGCGCTCGCGCTGGAG 1722
QY 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
DB 1723 AAGCGCGCAAGTACCGGTGCGCTCCGCTACGCCACT-----GAGGCC 1767
QY 592 IlePheValGluHisSerGlySerHisIleValSerPhePheAspCysSerAsnSer 611
DB 1768 GACATCGTGTCTCACGTGAACGACGCCAGATCCAG-----ATGCCCAAG 1812
QY 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
DB 1813 ACCATGAACCCCGCGAGGACCTCACCTCCAAGACCTTCAAGTGTGCGCGACCATCACC 1872
QY 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
DB 1873 ACCCTCAACCTCGCCACGACCTCTCTCGCCCTCAAGCAACACTCGCGGAGGACCCC 1932
QY 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn 662
DB 1933 AACTCCACCTCTCCGGCATCGTGTACGTGGACCGCATCGATTTCATCTCCCGTGGAC 1989
RESULT 15
US-10-032-717-15
; Sequence 15, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sins
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: Pesticidal Activity Against Coleopterans
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIORITY FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-10-032-717-15
Alignment Scores:
Pred. No.: 3,748-94 Length: 2010
Score: 526.00 Matches: 239
Percent Similarity: 50.8% Conservative: 116
Best Local Similarity: 34.2% Mismatches: 268
Query Match: 25.7% Indels: 76

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Search completed: January 21, 2006, 04:23:59

Job time : 1474 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 20, 2006, 23:21:18 ; Search time 296 Seconds

(without alignments)
1899.170 Million cell updates/sec

Title: US-10-782-096-2

Perfect score: 3597

Sequence: 1 MNSYKKNQYEMLDALRINS.....TPPNQSLKREQEVNDLFN 682

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 6049916 seqs, 41213615 residues

Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA New -OPMT=fastap -SUFFIX=p2n.rnpbn -MINWATCH=0.1
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USRP=US10782096 @CGN 1 1 121 @runat 20012006 095216 24440
-NCPUS=6 -ICPU=3 -NO MAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:
1: /cgn2_6/ptodata/1/pubpna/US08 NEW PUB.seq:
2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:
5: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10 NEW PUB.seq:
7: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq:
9: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq:
11: /cgn2_6/ptodata/1/pubpna/US60 NEW PUB.seq:

Added. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	26.4	3621	8	US-11-058-727-1 Sequence 1, Appl
2	948	26.4	3621	8	US-11-058-727-1 Sequence 1, Appl
3	948	26.4	4874	8	US-11-058-727-17 Sequence 17, Appl
4	948	26.4	4874	8	US-11-058-727-17 Sequence 17, Appl
5	926	25.7	2010	8	US-11-058-727-5 Sequence 5, Appl
6	926	25.7	2010	8	US-11-058-727-11 Sequence 11, Appl
7	926	25.7	2010	8	US-11-058-727-5 Sequence 5, Appl

8	926	25.7	2010	8	US-11-058-727-11	Sequence 11, Appl
9	925.5	25.7	2022	8	US-11-058-727-49	Sequence 49, Appl
10	925.5	25.7	2022	8	US-11-058-727-81	Sequence 81, Appl
11	925.5	25.7	2022	8	US-11-058-727-81	Sequence 49, Appl
12	925.5	25.7	2022	8	US-11-058-727-81	Sequence 81, Appl
13	925	25.7	2022	8	US-11-058-727-7	Sequence 7, Appl
14	925	25.7	2022	8	US-11-058-727-25	Sequence 25, Appl
15	925	25.7	2022	8	US-11-058-727-29	Sequence 29, Appl
16	925	25.7	2022	8	US-11-058-727-33	Sequence 33, Appl
17	925	25.7	2022	8	US-11-058-727-69	Sequence 69, Appl
18	925	25.7	2022	8	US-11-058-727-69	Sequence 69, Appl
19	925	25.7	2022	8	US-11-058-727-25	Sequence 25, Appl
20	925	25.7	2022	8	US-11-058-727-29	Sequence 29, Appl
21	925	25.7	2022	8	US-11-058-727-33	Sequence 33, Appl
22	925	25.7	2022	8	US-11-058-727-69	Sequence 69, Appl
23	924.5	25.7	2022	8	US-11-058-727-43	Sequence 43, Appl
24	924.5	25.7	2022	8	US-11-058-727-75	Sequence 75, Appl
25	924.5	25.7	2022	8	US-11-058-727-43	Sequence 43, Appl
26	924.5	25.7	2022	8	US-11-058-727-75	Sequence 75, Appl
27	924	25.7	2025	8	US-11-058-727-45	Sequence 45, Appl
28	924	25.7	2025	8	US-11-058-727-77	Sequence 77, Appl
29	924	25.7	2025	8	US-11-058-727-45	Sequence 45, Appl
30	924	25.7	2025	8	US-11-058-727-77	Sequence 77, Appl
31	924	25.7	3633	8	US-11-058-727-3	Sequence 3, Appl
32	924	25.7	3633	8	US-11-058-727-3	Sequence 3, Appl
33	924	25.7	6613	8	US-11-058-727-18	Sequence 18, Appl
34	924	25.7	6613	8	US-11-058-727-18	Sequence 18, Appl
35	920	25.6	2025	8	US-11-058-727-79	Sequence 79, Appl
36	920	25.6	2025	8	US-11-058-727-79	Sequence 79, Appl
37	920	25.6	2025	8	US-11-058-727-47	Sequence 47, Appl
38	920	25.6	2025	8	US-11-058-727-79	Sequence 79, Appl
39	916	25.5	2022	8	US-11-058-727-21	Sequence 21, Appl
40	916	25.5	2022	8	US-11-058-727-63	Sequence 63, Appl
41	916	25.5	2022	8	US-11-058-727-65	Sequence 65, Appl
42	916	25.5	2022	8	US-11-058-727-67	Sequence 67, Appl
43	916	25.5	2022	8	US-11-058-727-21	Sequence 21, Appl
44	916	25.5	2022	8	US-11-058-727-63	Sequence 63, Appl
45	916	25.5	2022	8	US-11-058-727-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-11-058-727-1
; Sequence 1, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis

FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)... (3621)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)... (0)
; OTHER INFORMATION: Cry1218-1
US-11-058-727-1

Alignment Scores:

Prod. No.: 4.05e-102 Length: 3621
Score: 948.00 Matches: 248
Percent Similarity: 50.9% Conservative: 119
Best Local Similarity: 34.4% Mismatches: 276
Query Match: 26.4% Indels: 78
DB: 8 Gaps: 25

US-10-782-096-2 (1-682) x US-11-058-727-1 (1-3621)

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DB 4 AGTCCAAATAATCAAAATGAATATGAATATAGATGCGACACCT---TCTACTTCTGTA 60
QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
DB 61 TCCAAATGATCTTAACACAGATACCTTTTGGAAATGACCCAAATGCGGTACAAATATG 120
QY 43 AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
DB 121 GATTATAAAGATTATTTAAATATGCTCT-----CGCGGAAATGCTAGT 162
QY 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
DB 163 GAATACCTCGTGGTTCACCTGAAGTACTTGTAGCGGACAGATGACGTAAAGCGCGCAAT 222
QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheDly 101
DB 223 GATATAGTAGTAATATCTATCAGGTTTGGGGTCCCATTTGTTGGGCGGATAGTACT 282
QY 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
DB 283 CTTTATACCTCAACTTATGATATCTGTGGCTTTCAGGCGAAAGAGTCAATGGGAAAT 342
QY 120 LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
DB 343 TTTATGGAACAAGTAGAAGACTCATTAATCAAAATAATAGCAATATGCAAGGAATAAA 402
QY 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
DB 403 GCGCTTCGGAATTAGAAGATTAGTAAATATACCAATATATCTAATCGCGCTTAA 462
QY 160 AlaTrpLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
DB 463 GAATGGGAAGAAATCCAAATGGTTCAAGAGCGCTTACGAGATGTGCGAAATCGATTGAA 522
QY 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnGluIle 198
DB 523 ATCTCGGATAGTTATTTAGCAATATATGCGCATCTTTTAGAGTGAACAATTTTGAAGTA 582
QY 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
DB 583 CCATTCCTTACTGTATATGCAATGGCAGCCCACTTCAATTTACTGTATTAAAGGACGCG 642
QY 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
DB 643 TCAATTTTGGAGAAGATGGGATGGTCAACAACACTACTATTAAATAACTATTATGATCGT 702
QY 239 LeuGlnGlyIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
DB 703 CAAATGAACCTTACTGCAGAAATTTCTGATCACTGTGTAAAGTGGTATGAACTGGTTTA 762
QY 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
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QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
DB 823 ATGACACTGGCGGTTTATAGATGTTTGCATTATTCCCAAAATATTGACACACGACGATAC 882
QY 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
DB 883 CCNATGGAAACGAAGACCACTAAACAGGAGATATATACAGATCCACTGGCGCGGTA 942
QY 319 GlyValLeuGluSerGlyGlyArgThrTyrProTrpTyrAsnProAsnAsnThrThrPhe 338
DB 943 AACGTGTCTTCAATTTGGTTCC-----TGGTATGAC---AAAGCACCTTCTTTC 987
QY 339 ThrAlaMetGluAsnAsnAlaArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
DB 988 GGAGTGATAGATCATCCGTTATTTCGACCACCCCATGTATTGTATTATATAACGGGACTC 1047
QY 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
DB 1048 ACAGTGTATACCAATCAAGAGCATTTCTCCGCTCGCTATATTAAGACAT---TGGGCT 1104
QY 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
DB 1105 GGTCAATCAAAATAGCTACCATCGTGTAGTAGGCTAGTAATCTTCAACAATAATGTATGA 1164
QY 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
DB 1165 ACTAATCAAAATCTACACAGCACTAGTACCTTTGTATTTTACGAATTTATGATATTACAAG 1224
QY 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
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QY 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
DB 1276 ---TATATATT---TTTGAATGCCAGAAGTCGAGTGTTCATGTGTAACCAATTTG 1326
QY 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
DB 1327 AATAATACCAGAAAGACGTTAAATGAT-----AATCCAGTTTCCAAAGATATT 1374
QY 470 LeuSer-----GluLeuProGlyLysAspLysProArgProAsn 482
DB 1375 ATAGCGAGTACAAGAGATTCGGAATTAGAATTACTCCAGAACTTCAGATCAACCAAT 1434
QY 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer 502
DB 1435 TATGAGTCATATAGCCATAGATTATGTATCATATCACAAGTATTCCCGCGACGGTAACACT 1494
QY 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn 522
DB 1495 ACCGGATTAGTACCT-----GTATTTCTTGGACACATCGAAGTCGAGATTAAAC 1545
QY 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn 542
DB 1546 AATACATATATTTCAGATAAATCACTCAATTCGCGCGCTTAATTTGG---GATAAT 1602
QY 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal 558
DB 1603 TTACCGTTTGTTCAGTGTAAAGGACCAAGACATACAGGAGGGGATTTATTACAGTAT 1662
QY 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
DB 1663 AATAGAAGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCCTAGCTTAGAA 1722
QY 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
DB 1723 AAAGCAGGGAATATCTGTAGATCTGAGATATGCTACT-----GATGCA 1767
QY 592 IlePheValGluHisSerGlySerHisIleValSerPhePheAspCysSerAsnSer 611
DB 1768 GATATTGTATTGCTGTAACGATGCTCAGATTTCAG-----ATGCCAAA 1812
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Db 1073 TTTATGGAACTAGAGAACTCATTAAATCAAAAATAGCAGATATGCAAGGAATATA 1132
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Db 1133 GCGCTTTTCGGAATAGAGGATAGTAATAATTACCAATTATATCTAACTCGCTTGA 1192
Qy 160 AlaTyrLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
Db 1193 GAATCGGAAGAAATCCAAATCGTTCAAGAGCGCTTACGAGATGTGCGAAATCGATTGA 1252
Qy 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
Db 1253 ATCTCGGATAGTTATTTACGCAATATATGCGCATCTTTAGAGTGACAAATTTGAGTA 1312
Qy 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
Db 1313 CCATTCTTACTGTATGATGCAATGGCAGCCAACTTCAATTTGTTTAAAGGACGCG 1372
Qy 219 AspTyrPheGlyAlaGlnTyrGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
Db 1373 TCAATTTTGGAGAAAGATGGGGATGGTCAACAACACTACTATTAACTATTTATGATCGT 1432
Qy 239 LeuGlnGlyLeuIleArgGlnTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 1433 CAATGAAACTTACTGCGAATATTTCTGATCACTGTGTAAGATGGTATGAAACTGGTTA 1492
Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp 278
Db 1493 GCAAAATTAAGGACGAGCGCTAAACAATGGTTGACTATAACCAATTCGTTAGAGAA 1552
Qy 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 1553 ATGACACTGGCGGTTTGTAGATGTGTGATTTATTCCTCAATTTATCCAAATTTATGACACGCGACTAC 1612
Qy 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
Db 1613 CCATGGAAACGAACGACACTAAACAGGGAAGTATATACAGATCCACTGGGCGCGTA 1672
Qy 319 GlyValLeuGluSerGlyGlyArgThrTyrProTyrAsnProAsnAsnThrThrPhe 338
Db 1673 AAGTGCTCTCAATTTGGTTCC-----TGGTATGAC---AAGCACCTTCCTTC 1717
Qy 339 ThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrThrThrLeuAsnArgIle 358
Db 1718 GAGTGATAGATATCATCGGTTATTCGACCCATCCATGATTTGATTTATATATACCGGATC 1777
Qy 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTyrGly 376
Db 1778 ACAGTGATATACAAATCAAGAAAGCATTTCTCCGCTCGCTATATAAGACAT---TGGGCT 1834
Qy 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
Db 1835 GGTCAATCAATAGCTACCATCGTCTCAGTAGGGGTAGTAACTTCAACAATGTATGA 1894
Qy 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
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Qy 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
Db 1955 ACTCTATCAAGAGATGCACTACTCTTGATATTTTACCCCTGGTTATACG----- 2005
Qy 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
Db 2006 ---TATATATTT-----TTTGGATGCCAGAGTCGAGTTTTCATGTTAAACCAATG 2056
Qy 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
Db 2057 AATAATACCAGAAAGACGTTAAAGTAT-----AATCCAGTTTCCAAAGATATT 2104
Qy 470 LeuSer-----GluLeuProGlyLysAspLysPheProArgProAsn 482
Db 2105 ATAGCGAGTACAAAGAGATTCGGAAATTAGAAATTACCTCCAGAAACTTCAGATCAACCAAT 2164

Qy 493 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer 502
Db 2165 TATGAGTCATATAGCCATAGATTATGTATCATACAAAGTATTTCCCGCGACGGTAACACT 2224
Qy 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn 522
Db 2225 ACCGATTTAGTACCT-----GTAATTTCTTGGACACATCGAAGTCGAGATTTAAAC 2275
Qy 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyGlyAsn 542
Db 2276 AATCAATATATTCAGATAAATCACTCAATTCGCGCGTTAAATGTTGG---GATAT 2332
Qy 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal 558
Db 2333 TTACCGTTTGTTCAGTGTAAGGACGAGCATACAGAGGGGATTTATTACAGTAT 2392
Qy 559 SerAspSerTyrHisSerLeuLysVal-----GlnAlaProGln 571
Db 2393 AATAGAAGTACTGGTTCTGTAGGAACCTTATTTAGCTCGATATGGCCTAGCATTAGAA 2452
Qy 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 2453 AAAGCAGGGAATATCGTGTAAAGACTGAGATATGCTACT-----GATGCA 2497
Qy 592 IlePheValGluHisSerGlySerHisIleValSerPheAspCysSerAsnSer 611
Db 2498 GATATGTATTGTCATGTAACGATGCTCAGATTTCAG-----ATGCCAAA 2542
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 2543 ACAATGAACCCAGGAGGAGTCTGACATCTAAACATTTTAAAGTTGCAGATGCTATCACA 2602
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 2603 ACATTAATTTAGCAACAGATAGTTCGTAGCATTTGAAACATAATTTAGTGAAGACCT 2662
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 2663 AATCAACATATCTCGTATAGTTTACCTTGACCGAATCGAATTCATCCAGTAGTAG 2722
Qy 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
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Qy 682 Asn 682
Db 2783 AAT 2785

RESULT 4

US-11-108-389-17
; Sequence 17, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herxmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108.389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320


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QY 592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAenSer 611
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QY 612 SerGlyArgProSerAenThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 2543 ACAATGAACCCAGGTGAGATCTGACATCTAAACCTTTTAAAGTTGCAGATGCTATCACA 2602
QY 632 IlePheThrProSerIleAenProLeuIleArgTyrArg----- 644
Db 2603 ACATTAAATTAGACACAGATAGTTGCTAGCATTTGAAACATAATTTAGTGAAGCCCT 2662
QY 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAen--- 662
Db 2663 AATTCAACATTAATCTGCTATAGTTTACGTTGACCGAATCGAATTCATCCAGTAGATGAG 2722
QY 663 ThrPhe---ProAenGlnSerLeuLysArgGluGlnGluValAenAspLeuPheIle 681
Db 2723 ACATATGAAGCGGAAACAGATTTAGAAAGCAGCGAAGAAAGAGTGAATGCTTTGTACG 2782
* QY 682 Aen 682
Db 2783 AAT 2785
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RESULT 5

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US-11-058-727-5
; Sequence 5, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Ronald R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Li
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 357118/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; OTHER INFORMATION: Maize optimized Cry1218-1
; FEATURE:
; NAME/KEY: misc feature.
; LOCATION: (0)...(0)
; OTHER INFORMATION: mol218-1
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US-11-058-727-5

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Alignment Scores:
Pred. No.: 6,54e-100 Length: 2010
Score: 926.00 Matches: 239
Percent Similarity: 50.8% Conservative: 116
Best Local Similarity: 34.2% Mismatches: 268
Query Match: 25.7% Indels: 76
DB: 8 Gaps: 23
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US-10-782-096-2 (1-682) x US-11-058-727-5 (1-2010)
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Db 4 TCCCCCAACACAGACGAGTACGAGATCATCGACGCCACCCCC---TCCACCTCCGCG 60
QY 23 SerAenCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAenThr 42
Db 61 TCCAACGACTCCACACGCTTACCCCTCGCCCAACGAGCCCAACACGCCCTCCAGAATCATG 120
QY 43 AenTyrLysGluTyrProLeuAenMetCysAspSerAenThrGlnPheIleGlyAspIleSer 62
Db 121 GACTACAAAGGACTACCTCAAGATGTC-----GCCGSCAACACGCTCC 162
QY 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 163 GAGTACCCCGGCTCCCGAGGTGCTGTCGCCGAGGAGCGCCGCAAGCGCCCATC 222
QY 82 AenSerValGlyThrIleLeuSerAenLysValProLeuAlaSerGlnSerPheGly 101
Db 223 GACATCGTGGGCAAGCTCTCTCGGCTCGGCGTGCCTTCGTGGGCCCATCGGTGCC 282
QY 102 IleIleSerArgLeuIleGlyIleLeuTyrAlaGlyProAsp-----ProPheGluAla 119
Db 283 CTCTACACCCAGCTCATCGACATCTCTGGCCCTCGCGAGAGTCCCGAGTGGGAATC 342
QY 120 LeuMetValLeuValGluLeuIleLysLysSerIleAenGlnArgValArgGluAen 139
Db 343 TTCATGGAGCAGGTGGAGAGCTCATCAACAGAGATCGCGAGTACGCCGCCAACAAAG 402
QY 140 AlaLeuArgGluLeuGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 403 GCCCTCTCCGAGCTGGAGGGCTCGGCAACACTACAGCTCTACTCTCACCCTCCGAG 462
QY 160 AlaTyrLeuValAenLysAenAspAenArg---ArgAlaLeuValThrGlnTyrAla 178
Db 463 GAGTGGGAGGAGAACCCCAACGGCTCCCGCGCCCTCCGCGAGTGGCAACCGCTTCGAG 522
QY 179 IleValAspAenPhePheGluLysAenMetProLysPheLysGluArgAenPheGluIle 198
Db 523 ATCTCGACTCCCTCTCACCAGTACATGCCCTCCTCCGCGTGACCAACCTTCGAGGTG 582
QY 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAenLeuHisLeuIleLeuLeuArgAspAla 218
Db 583 CCCTTCCTCACCCTGTAGCCCATGCGCCCAACCTCCACCTCTCTCTCTCAAGNAGCC 642
QY 219 AspTyrPheGlyAlaGlnTyrGlnLeuGlyAspGluIleArgAspAenTyrIleArg 238
Db 643 TCCATCTTCGCGAGGAGTGGGGCTGGTCCACCACCATCAACAACTACTACGACCCG 702
QY 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAenGlnGlyLeu 258
Db 703 CAGATGAAGCTCACCGCGAGTACTCCGACCATCGTGAAGTGGTATGAGACCGGCTTC 762
QY 259 AenGlnPheAenArgSerAenAlaGlnAspTyrValSerPheAenArgPheArgThrAsp 278
Db 763 GCCAAGCTCAAGGGCACCCTCCGCCAAGCAGTGGGTGGACTACACAGTTCGCCCGCGAG 822
QY 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAenTyrAspProArgTyr 298
Db 823 ATGACCTTCGCGTGTCTGACGTGGTGGCCCTTTCGCCCACTACGACACCCGCCACTAC 882
QY 299 ProLeuAlaValLysThrGluLeuValTyrArgGluValTyrThrAspProValGlyPheThr 318
Db 883 CCCATGGAGACCAAGGCCAGCTCACCAGCGAGGTGTACACGACCCGCTCGCGCGCGT 942
QY 319 GlyValLeuGluSerGlyGlyArgThrTyrProTyrTyrAenProAenAenThrThrPhe 338
Db 943 AACGTGTCTCCATCGGCTCT-----TGGTACGAC---AAGGCCCAAGCTTC 987
QY 339 ThrAlaMetGluAenAenAlaArgArgProSerTyrThrTyrThrLeuAenArgIle 358
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Db 988 GCGGTGATGAGTCTCCGTGATCGCGCGCGACGTGTTTCGACTACATCACCGCGCTC 1047
Qy 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly 376
Db 1048 ACCGGTACACAGTCCCGCTCCATCTCTCCGCGGTACATCCGCCAC---TGGGCC 1104
Qy 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
Db 1105 GGGCCACCATCTCTACACCGCGTGTCCCGGCTCAACCTCCAGCAGATGTACGGC 1164
Qy 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
Db 1165 ACCAACCCAGAACCTCCACCTCCACCTCCACCTTCGACTTCACCACTACGACATCAAG 1224
Qy 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyThrGluAlaAsn 430
Db 1225 ACCCTCTCAAGGACCGGTCTCTCGACATCGTGATCCCGGCTACACC----- 1275
Qy 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
Db 1276 ---TACATCTTC-----TTCCGATCGCGAGGTGGAGTTCTTCATGTGAACACGCTC 1326
Qy 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
Db 1327 AACAAACCCCGACAGACCTCAATAC-----AACCCCGTGTCCAAGGACATC 1374
Qy 470 LeuSer-----GluLeuProGlyLysAspLysProArgProAsn 482
Db 1375 ATCGGCTCCACCGGACTCCGAGTCCGAGCTCCCGCGGACCTCCGACCGACCAAC 1434
Qy 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgSerSer 502
Db 1435 TACGAGTCTACTCCACCGCTCTGCCACATCCTCCATCCCGCCACCGGACACAC 1494
Qy 503 SerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsn 522
Db 1495 ACCGGCTCGTCCG-----GTGTTCTCTGGACCCACCGCGGCGGACCTCTCCAGTAC 1545
Qy 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyGlyAsn 542
Db 1546 AACACATCTACTCCGACAGATACCCAGATCCCGCGCGTGAAGTGTGG---GACAAAC 1602
Qy 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal 558
Db 1603 CTCCCTTCGTGCTCGTGTGAAGGCGCCCGCACACCGCGGCGGACCTCTCCAGTAC 1662
Qy 559 SerAspSerTrpHisSerLeuLysVal-----GlnAlaProGln 571
Db 1663 AACCGCTCCACCGGCTCCGTGGGCACCTCTTCCTCGCGCGCTACGGCTCCCGCTGGAG 1722
Qy 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 1723 AAGGCGGGAAGTACCGGTGCGCTCCGCTACGCCACT-----GACGCC 1767
Qy 592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
Db 1768 GACATCGTGCTCCAGTGNACACGCCCGCCAGATCCAG-----ATGCCCAAG 1812
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 1813 ACCATGAACCCCGGCGAGACCTCACCTCAAGACCTTCAAGTGGCGGACCCATCAC 1872
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 1873 ACCCTCAACCTCGCCACGACTCTCTCTCGCCCTCAAGCAACACCTCGCGGAGACCCC 1932
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn 662
Db 1933 AACTCCACCTCTCCGGCATCGTGATCGTGGACCGCATCGATTCATCCCGCTGGAC 1989
RESULT 6
US-11-058-727-11
; Sequence 11, Application US/11058727
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; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-11-058-727-11
Alignment Scores:
Pred. No.: 6,54e-100 Length: 2010
Score: 926.00 Matches: 239
Percent Similarity: 50.8% Conservative: 116
Best Local Similarity: 34.2% Mismatches: 268
Query Match: 25.7% Indels: 76
DB: 8 Gaps: 23
US-10-782-096-2 (1-682) x US-11-058-727-11 (1-2010)
Qy 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 4 AGTCCAAATAATCAAAATGAATATGAAATTATAGTGCACACCT---TCTACTTCTGTA 60
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 61 TCCAATGATTCTTAACAGATACCTTTTCGGAATGCGCCAAATGCGCTACAAATATG 120
Qy 43 AsnTyrLysGluTyrLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 121 GATTATAAGATTATTTAAATGTCT-----GCCGGAAATGCTAGT 162
Qy 63 ThrTyr---SerSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 163 GAATACCCCTGTTTCCCTGAAAGTACTTGTAGCGACAAGATGCAAGCTAAGCGCCCAATT 222
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 223 GATATAGTAGTAAATTAATACTATCAGTTTAGGGTCCCATTTTGTGGCCGATAGTAGT 282
Qy 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----PropheGluAla 119
Db 283 CTTTATACTCAACTTATTTGATATTTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAATT 342
Qy 120 LeuMetValLeuValGluGluLeuIleLysSerIleAspGlnArgValArgGluAsn 139
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Db 343 TTTATGGAACAAGTAGAAGAACTCATTAAATCAAAAATAGCAGAAATATCGAAGATATA 402
Qy 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 403 GCGCTTCGGAATAGAGGAATAGGTAATAATACCAATATATATCAACTCGCGCTGAA 462
Qy 160 AlaTyrLeuValAsnLeuAspAspAspAspAspAspAspAspAspAspAspAspAsp 178
Db 463 GAATGGGAAGAAATCCAAATGGTTCAGAGCCTTACGAGATGTGGGAATCGATTGAA 522
Qy 179 IleValAspAspPhePheGluLeuAsnMetProLysPheLysGluArgAsnGluIle 198
Db 523 ATCTCGATAGTTTATTAACGCAATATATGCCATCTTTAGAGTGACAAATTTGAGTA 582
Qy 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuLeuLeuLeuLeuLeu 218
Db 583 CCATCTCTACTGTATGATGCAATGGCGACCAACCTTCATTACTGTATTAAGGACGG 642
Qy 219 AspTyrPheGlyAlaGlnTyrGlnLeuGlyAspAspGluLeuArgAspAspTyrIleArg 238
Db 643 TCAATTTTGGAGAAAGATGGGATGGTCAACAACCTACTATTAAATAACTATTATGATCGT 702
Qy 239 LeuGlnGlyLeuLeuArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 703 CAATGAACCTTACTGCAGATATCTGATCACTGTGTAAGTGGTATGAACCTGGTTTA 762
Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp 278
Db 763 GCAAAATTAAGGACGAGCGCTAAACAATGGTTGACTATATAACCAATTCGTAGAGAA 822
Qy 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 823 ATGACACTCGCGGTTTATAGTGTGTGATATTATCCCAAAATATGACACACGACGTAC 882
Qy 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrAspProValGlyPheThr 318
Db 883 CCATGGAAACGAAGCACAACCTAACAGGAAGTATATACAGATCCACTGGCGCGGTA 942
Qy 319 GlyValLeuGluSerGlyGlyArgThrTyrProTyrPyrAsnProAsnAsnThrPhe 338
Db 943 AACGTGTCTCAATGGTTCC-----TGGTATGAC--AAAGCACCTTCCTTC 987
Qy 339 ThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrThrThrLeuAsnArgIle 358
Db 988 GGAGTGATAGATCATCCGTTTATCGACCACCCCATGTATTTGATTTATATAACGGGACTC 1047
Qy 359 PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTyrGly 376
Db 1048 ACAGTGATACACAATCAAGAAGCACTTCTCCGCTCGCTATATAGACAT---TGGGCT 1104
Qy 377 GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly 395
Db 1105 GGTCAATCAATAGCTACCATCGTGCAGTAGGGTAGTAATCTTCAACAATGTATGGA 1164
Qy 396 LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer 415
Db 1165 ACTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATATATGATATTTACAAG 1224
Qy 416 IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn 430
Db 1225 ACTCTATCAAGAGATGCACTCTCTTGATATTTGTTTACCCTGGTTATACG----- 1275
Qy 431 AsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIle 449
Db 1276 ---TATATATTT-----TTTGGATGCCAAGTCGAGTTTTCATGTTAAACCAATG 1326
Qy 450 AsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIle 469
Db 1327 AATAATACCAGAAGACGTTAAAGTAT-----AATCCAGTTTCCAAGATATT 1374
Qy 470 LeuSer-----GluLeuProGlyLysAspLysProArgProAsn 482
Db 1375 ATAGCGAGTACAGAGATTCCGAATTTAGAAATTTACCTCCAGAAACTTCAGATCAACCAAT 1434

Qy 483 AlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSer 502
Db 1435 TATGAGTCATATAGCCATAGATATTGTCTATATCACAAGTATTCGCCGACGGGTAACT 1494
Qy 503 SerGlyGlyIleValSerLeuThrPheGlyTyrAlaHisThrSerMetAspArgAsn 522
Db 1495 ACCGATTTAGTACT-----GTATTTCTTGACACATCGAAGTCGAGATTTAAAC 1545
Qy 523 AsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTyrGlyGlyAsn 542
Db 1546 AATACAATATATTCAGATAAAATCACTCAAAATTCGCGCGTTAAATGTTGG---GATAAT 1602
Qy 543 IleGlyPheValIle-----ProGlyProThrGlyGlyAsnLeuValLysVal 558
Db 1603 TTACCGTTTGTTCCTAGTGGTAAAGCACGAGACATACAGAGGGGATTTATTACAGTAT 1662
Qy 559 SerAspSerTyrPheHisSerLeuLysVal-----GlnAlaProGln 571
Db 1663 AATAGAGTACTGGTTCGTAGGAACCTTATTTCTAGCTCGATATGGCCTAGCATTAGAA 1722
Qy 572 ArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAla 591
Db 1723 AAAGCAGGGAATATCTGTAGACTGAGATATGCTACT-----GATGCA 1767
Qy 592 IlePheValGluHisSerGlySerHisIleValSerPhePheAspCysSerAsnSer 611
Db 1768 GATATTGTATTGCTGATTAACGATGCTCAGATTGCTAG-----ATGCCAAA 1812
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 1813 ACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCAGATGCTATCACA 1872
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 1873 ACATTAATTTAGCAACAGATAGTTTCGTAGCATTTGAACATAATTTAGTGAAGACCCT 1932
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn 662
Db 1933 AATCAACATTTATCTGGTATAGTTTACGTTGACCAATCGAATTCATCCAGTAGAT 1989
RESULT 7
US-11-108-389-5
; Sequence 5, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

Qy	3	SerTyrIysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet	22
Db	4	AGTCCAAATATCAAAATGAATATGAAATATAGATGCGACACCT---TCTACTTCTGTA	60
Qy	23	SerAsnCySivTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr	42
Db	61	TCCAAATGATTCACAGATACCCCTTTGCGAATGAGCCAAACAAATGCGCTACAAATATG	120
Qy	43	AsnTyrLysGluTyrProLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer	62
Db	121	GATTATAAGATTATTAATAATGTCT-----GCGGGAAATGCTAGT	162
Qy	63	ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle	81
Db	163	GAATACCTCGTTCACCTGGAAGTACTTTGTAGCGGACAAAGATGCGACTAAGCGCGCAATT	222
Qy	82	AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly	101
Db	223	GATATAGTAGTAAATTAATCATCAGTTTAGGGTCCCAATTTGTTGGGCCGATAGTAGT	282
Qy	102	IleIleSerArgLeuIleGlyIleLeuTyrAlaGlyProAsp-----ProPheGluAla	119
Db	283	CTTTATACTCAACTTATTGATATTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAATT	342
Qy	120	LeuMetValLeuValGluGluLeuIleLysSerIleAspGlnArgValArgGluAsn	139
Db	343	TTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATATAGCAGAATATATGCAAGGAATAA	402
Qy	140	AlaLeuArgGluLeuGluGluGluGluGluIleMetArgLeuTyrGlnThrArgLeuGln	159
Db	403	CGCGTTTCGGAAATTAGAAAGGATAGGTAAATTAATCAACCAATTATATCTCAACTGCGCTTGA	462
Qy	160	AlaTrpLeuValAsnLysAsnAspAsp-----AsnArgArgAlaLeu-----	173
Db	463	GAATGGGAAGAAAAATCCAAATGGTTCGCGGTTCGAGTGCACAAGCCTTACGAGATGTG	522
Qy	174	ValThrGlnTyrAlaIleValAspAsnPhePheGluLysAsnMetProLysPheLysGlu	193
Db	523	CGAAATCCGATTTGAAATCTCGATAGTTTATTATCGCAATATATATGCCACTCTTTAGATG	582
Qy	194	ArgAsnPheGluIleLeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIle	213
Db	583	ACAAATTTTGAAGTACCACTTCCTTACTGTATATGCAATGGCAGCAACCTTCATTTACTG	642
Qy	214	LeuLeuArgAspAlaAspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArg	233
Db	643	TTATTAAAGACGCGTCAAATTTTGGAGAAGAAATGGGGATGGTCAACAACCTACTATTAA	702
Qy	234	AspAsnTyrIleArgLeuGlnGlyIleLeuArgGluTyrLysAspHisCysIleThrPhe	253
Db	703	AACATTATTGATCGTCAAAATGAAACTTACTCGAGAATATTCGTGATCACTGTGTAAAGTGG	762
Qy	254	TyrAsnGlnGlyLeuAsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsn	273
Db	763	TATGAAACTGGTTTATGCAAAATTAAGGACGACGCGCTAACCAATGGGTTCAGTATAAC	822
Qy	274	ArgPheArgThrAspMetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyr	293
Db	823	CAATTCGGTAGAAGAAATGACACTGGCGGTTTTAGATGTTGTGTGCAATTATTCCTCAAAAT	882
Qy	294	AspProArgArgTyrProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAsp	313
Db	883	GACACGCGACGTACCCCAATGGAAACGAAAGCACAACTTAACAGGGGAAGTATATACAGAT	942
Qy	314	ProValGlyPheThrGlyValLeuGluSerGlyArgThrTyrProTyrTyrAsnPro	333
Db	943	CCACTGGCGCGGTAAACGTGTCTCAATTGGTTCC-----TGATATGAC----	987
Qy	334	AsnAsnThrThrPheThrAlaMetGluAsnAsnAlaArgArgProSerTyrThrThr	353
Db	988	AAAGCACCTTCTTTTCGGAGTGAATAGATCACTCCGTATTTCACGACCCCAATGTTGAT	1047

Qy	354	TrpLeuAenArgIlePheValTyrThr-----ArgThrLeuGlyAenMetSerAspVal	371
Db	1048	TATATAACGGGAGCTCACAGTGTATATACAATCAAGAGACATTTCTCCGCTCGCTATATA	1107
Qy	372	ArgAenIleTrpGlyGlyHisThrLeu---ValGluAenGlyAenAspGlySerGluIle	390
Db	1108	AGACAT---TGGGCTGTGTATCAAAATAGCTACCATCGTCTCAGTAGGGGTAGTAATCTT	1164
Qy	391	ThrHisAenPheGlyLysThrAspSerIleThrProIleGlnTyrPheAenPheAlaAen	410
Db	1165	CAACAATGTATGGAACTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTTCAGAA	1224
Qy	411	LeuSerValPheSerIleGluSer-----LeuAlaArgIleTyrLeuGly	425
Db	1225	TATGATATTTACAAGACTCTATCAAAAGGATGCAGTACTCTTCATATTTTACCCCTGGT	1284
Qy	426	GlyThrGluAlaAenAenTyrIleThrSerGlnTyrGlyValSerArgVal----IlePhe	444
Db	1285	TATACG-----TATATATTT-----TTTGGAAATGCCAGAAGTCGAGTTTTC	1326
Qy	445	AsnThrSerAenIleAenAenValProGlySerLeuArgTyrGluValProAlaAenLeu	464
Db	1327	ATGGTAACCAATGAATATATACAGAAAGACGTTAAAGTAT-----AATCCA	1374
Qy	465	ProSerGlnThrIleLeuSer-----GluLeuProGlyLysAsp	477
Db	1375	GTITTCCAAAGATATATAGCGGTACAAAGATTCGGAATTAGAATTTACCTCCAGAACT	1434
Qy	478	LysProArgProAenAlaGlyAspPheSerHisArgLeuSerTyrIleSerAenPheAsp	497
Db	1435	TCAGATCAACCAAAATATGAGTCAATAGCATAGATATGTCATATCATCAAGATTAITCCC	1494
Qy	498	AlaArgArgSerSerGlyGlyIleValSerLeuLeuThrPheGlyTyrAlaHisThr	517
Db	1495	GCAGCGGTAACTACCGGATTAGTACCT-----GTATTTTCTCGACACATCGA	1545
Qy	518	SerMetAspArgAenAenArgLeuGluProAspLysIleThrGlnIleAspAlaValLys	537
Db	1546	AGTGCAGATTAAACATACAAATATATTCAGATAAATCACTCAATTCGGCGGTAAA	1605
Qy	538	GlyTrpGlyAenIleGlyPheValIle-----ProGlyProThrGlyGly	553
Db	1606	TGTTGG--GATAATTTACCGTTTGTTCAGTGTGTAAAGACGACGACATACAGGAGG	1662
Qy	554	AsnLeuValLysValSerAspSerTrpHisSerLeuLysVal-----	567
Db	1663	GATTTATTCAGTATATAGAGTACTGGTCTCTGTAGAACCTTATTTCTAGCTCGATAT	1722
Qy	568	--GlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuVal	586
Db	1723	GGCTACANTAGAAAAGCAGGGAATATCGTGTAGATGAGATATGCTACT-----	1776
Qy	587	ThrHisGlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPhePhe	606
Db	1777	-----GATGCAGATATTGTATTGTCATGTAAACGATGCTCAGATTTCAG-----	1818
Qy	607	AspCysSerAenSerSerGlyArgProSerAenThrLeuLeuGluSerAenPheArgTyr	626
Db	1819	-----ATGCCAAAAACAATGAACCCAGGTGAGGATCTGCACATCTAAACTTTTAAAGTT	1872
Qy	627	IleAspValProGlyIlePheThrProSerIle-----AsnProLeuIleArg	642
Db	1873	GCAGAT-----GCTATCAACAACGTTAAATTTAGCAACAGATAGTTCGGTTGCAGTTAAA	1926
Qy	643	Tyr-----ArgThrGlnSerPheGlyThrHisAlaIleAspLysPhe	656
Db	1927	CATAATTTAGTGAAGACCCCTAATTCACAACATATCTGGTATAGTTCAGTTGACCGAATC	1986
Qy	657	GluPheIleProLeuAen	662
Db	1987	GAATTCATCCGATAGAT	2004

RESULT 11

US-11-108-389-49
; Sequence 49, Application US/11108389
; Publication NO. US20050261188A1
; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu

; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity

; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389

; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786

; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787

; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320

; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49

; LENGTH: 2022
; TYPE: DNA

; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (1) ... (2022)

US-11-108-389-49

Alignment Scores:
Pred. No.: 7,6e-100 Length: 2022
Score: 925.50 Matches: 243
Percent Similarity: 51.3% Conservative: 119
Best Local Similarity: 34.4% Mismatches: 259
Query Match: 25.7% Indels: 85
DB: 8 Gaps: 26

US-10-782-096-2 (1-682) x US-11-108-389-49 (1-2022)

QY 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
DB 4 AGTCCAAATATCAAAATGAATGAAATTTATAGATGCGACACCT---TCTACTTCTGTA 60
QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
DB 61 TCCAAATGATCTTAACAGATACCTTTTGGCAATGAGCCAAACAAATGCGCTACAAATATG 120
QY 43 AsnTyrLysGluTyrProLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
DB 121 GATTATAAGATATTTAAAAATGTCT-----GCGGGAAATGCTAGT 162
QY 63 ThrTyr---SerSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
DB 163 GAATACCTCGTGTTCACAGTACTTGTGTAGCGACAGATGCGAGTAAAGCCCGCAATT 222
QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
DB 223 GATATAGTAGGTAATTAATCTATCAGTTTGGGGTCCCATTTTGTGGGCGGATAGTGTAGT 282
QY 102 IleIleSerArgLeuIleGlyIleLeuThrAlaGlyProAsp-----ProPheGluAla 119
DB 283 CTTTATACCTCAACTATTGATATTCTGTGGCTTCAGGGGAAAGAGTCAATGGCAATT 342
QY 120 LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
DB 343 TTTATGGCAAGTAGAAGAACTCATTAATCAAAAAATAGCAGAAATATGTCAGGAATAAAA 402

QY 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
DB 403 GCGCTTTCGGAATTAGAAGGATTAGGTAATAATTAACCAATTATATCTAACTCGCGTTGAA 462
QY 160 AlaTyrLeuValAsnLysAsnAspAsp-----AsnArgArgAlaLeu----- 173
DB 463 GAATGGGAAGAAATCCAAATGGTTCCCGGTTTCGAAGTCGACAAAGCCTTACGAGATGTG 522
QY 174 ValThrGlnTyrAlaIleValAspAsnPhePheGluLysAsnMetProLysPheLysGlu 193
DB 523 CGAAATCGATTGAAATCTCGATAGTTATTATTACGCAATATATGCCATCTTTTAGAGTG 582
QY 194 ArgAsnPheGluIleLeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIle 213
DB 583 ACAAAATTTGAAGTACCATTCTTACTGTATATGCAATGGCAGCCCAACCTTCATTACTG 642
QY 214 LeuLeuArgAspAlaAspTyrPheGlyAlaGlnTyrGlnLeuGlyAspGluIleAsG 233
DB 643 TTATTAAAGGACGCGTCAATTTTGGAGAAGNAATGGGATGGTCAACAACACTACTATTAT 702
QY 234 AspAsnTyrIleArgLeuGlnGlyLeuIleArgGluTyrLysAspPheCysIleThrPhe 253
DB 703 AACTATTATGATCGTCAAAATGAAACTTACTGCAGAAATATCTCGATCAGTGTGTAAGTGG 762
QY 254 TyrAsnGlnGlyLeuAsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsn 273
DB 763 TATGAAACTGGTTTAGCAAAATTTAAAGGCACAGCGCTAAACAATGGGTGCACTATAAC 822
QY 274 ArgPheArgThrAspMetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyr 293
DB 823 CAATTCGCTAGAGAAATGACACTGGCGGTTTATAGATGTTTGGCAATATTTCCTCAATAT 882
QY 294 AspProArgArgTyrProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAsp 313
DB 883 GACACACGCGCTACCCCAATCGAAACGAAAGCACAACCTAAACAAGGAGATATATACAGAT 942
QY 314 ProValGlyPheThrGlyValLeuGluSerGlyGlyArgThrTyrProTyrTrpAsnPro 333
DB 943 CCACCTGGGCGGTTAAACGCTGTCTTCAATTTGGTTCC-----TGGTATGAC---- 987
QY 334 AsnAsnThrThrPheThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrThr 353
DB 988 AAAGCACCTCTCTTCGGAGTGATAGATCATCGTTATTTCGACCACCCCATGTTTGTAT 1047
QY 354 TrpLeuAsnArgIlePheValTyrThr-----ArgThrLeuGlyAsnMetSerAspVal 371
DB 1048 TATATAACGGGACTCAGAGTGTATACACAATCAAGAGCAATTTCTCGCTCGCTATATA 1107
QY 372 ArgAsnIleTyrGlyGlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIle 390
DB 1108 AGACAT---TGGGCTGGTCAATCAATAAGCTACCATCGTGTGAGTGGGTAGTAACTCTT 1164
QY 391 ThrHisAsnPheGlyLysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsn 410
DB 1165 CAACAAATGTATGGAACCTTAATCAAAATCTACACAGCAGTAGTACCTTTGATTTTACGAAT 1224
QY 411 LeuSerValPheSerIleGluSer-----LeuAlaArgIleTyrLeuGly 425
DB 1225 TATGATATTTACAGACTCTATCAAGAGTGCAGTACTCTCTTGATATTTGTTACCTGGT 1284
QY 426 GlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePhe 444
DB 1285 TATACG-----TATATATTT-----TTTGGAAATGCCAGAGTCGAGTTTTTTC 1326
QY 445 AsnThrSerAsnIleAsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeu 464
DB 1327 ATGTGTAACCAATTAATTAATCAACGAAAGAGCTTTAAAGTAT-----AATCCA 1374
QY 465 ProSerGlnThrIleLeuSer-----GlutLeuProGlyLysAsp 477
DB 1375 GTTTCGAAGATATTTATGCGGATACAGAGATTCGGAATTAAGATTTACCTCCAGAACT 1434
QY 478 LysProArgProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAsp 497

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Db 1435 TCAGATCAACCAATATGAGTCATATAGCCATAGATTATGTCATATCACAAGTATTCCTC 1494
Qy 498 AlaArgArgSerSerGlyGlyLeuValSerLeuLeuThrPheGlyTrpAlaHisThr 517
Db 1495 GCGACGGGTAAACATACCGGATTAGTACCT-----GTATTTCTTGGACACATCGA 1545
Qy 518 SerMetAspAsnAsnArgLeuGluProAspGlyLeuThrGlnLeuAspAlaValLys 537
Db 1546 AGTCAGATTAAACACATACATATATTCAGATAAATACCTCAAAATCCGGCCGTTAAA 1605
Qy 538 GlyTrpGlyGlyAsnIleGlyPheValIle-----ProGlyProThrGlyGly 553
Db 1606 TGTTGG---GATAATTCAGTTTGTTCAGGTGTTAAAGGACACAGACATACAGAGGG 1662
Qy 554 AsnLeuValLysValSerAspSerTrpHisSerLeuLysVal----- 567
Db 1663 GATTTATTACAGTATAATAGAAAGTACTGGTCTCTAGGAACCTTATTTCTAGCTCGATAT 1722
Qy 568 ---GlnAlaProGlnArgGlnThrSerTrpArgIleArgLeuArgTrpAlaCysLeuVal 586
Db 1723 GGCCTAGCATTTAGAAAAGACGGGAAATATCTGTGAAGACTGAGATATGCTACT----- 1776
Qy 587 ThrHisGlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPhePhe 606
Db 1777 -----GATGACAGATATTGTATTCATGTAAACGATGCTCAGATTTCAG----- 1818
Qy 607 AspCysSerAsnSerSerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTrp 626
Db 1819 -----ATGCCAAAACCAATGAACCGGTGAGGATCTGCATCTAAAACCTTTAAAGTT 1872
Qy 627 IleAspValProGlyIlePheThrProSerIle-----AsnProLeuIleArg 642
Db 1873 GCAGAT-----GCTATCAACAGTTAATTTAGCAACAGATAGTTCGGTTCAGTTAAA 1926
Qy 643 Tyr-----ArgThrGlnSerPheGlyThrHisAlaIleAspLysPhe 656
Db 1927 CATATGTAGGTGAAGACCTTAATTCACATTTATCTGGTATAGTTTACGTTGACCGCAATC 1986
Qy 657 GluPheIleProLeuAsn 662
Db 1987 GAATTCATCCAGTAGAT 2004
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RESULT 12

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US-11-108-389-81
; Sequence 81, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Preenail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2022
; TYPE: DNA
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; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2022)
US-11-108-389-81

Alignment Scores:
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Score: 925.50 Matches: 243
Percent Similarity: 51.3% Conservative: 119
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US-10-782-096-2 (1-682) x US-11-108-389-81 (1-2022)
Qy 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
Db 4 AGTCCAAATAATCAAAATGAATATGMAATTATAGATGCGACACCT---TCTACTTCTGTA 60
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 61 TCCAATGATTCTTAACAGATACCTTTTTCGGAATGAGCCAAACAAATGCCGTACAAAATATG 120
Qy 43 AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 121 GATTATAAAGATTATTTAAAAATGTCT-----GCGGGAATGTCTAGT 162
Qy 63 ThrTyr---SerSerProGluAlaAlaSerValArgAspAlaValLeuThrGlyIle 81
Db 163 GAATACCTCGTTCACCTGAAGTACTTGTGTAGCGACAAGATGCGAGTAAAGCCCAATT 222
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 223 GATATAGTAGGTAATATCTACTCAGTTTGGGGTCCCATTTGTTGGGCCGATAGTGTAGT 282
Qy 102 IleIleSerArgLeuIleGlyLeuTrpAlaGlyProAsp-----ProPheGluAla 119
Db 283 CTTTATACTCAACTTATTTGATATTTCTGTGGCCTTCAGGGGAAAGAGTCAATGGGAAATT 342
Qy 120 LeuMetValLeuValGluLeuIleLysSerIleAspGlnArgValArgGluAsn 139
Db 343 TTTATGGAAACAAGTAGAAGAACTCATTAAATCAAAAATAGCAGAATATGCAAGGAATAA 402
Qy 140 AlaLeuArgGluLeuGluGlyLeuMetArgLeuTyrGlnThrArgLeuGln 159
Db 403 GCGCTTTTCGGAATTAGAAGGATTAGTAATAATTTACCAATTTATATCTAACTCGCTTGA 462
Qy 160 AlaTrpLeuValAsnLysAsnAspAsp-----AsnArgArgAlaLeu----- 173
Db 463 GAATGGGAGAGAAATCCAAATGGTTCGCGTTTCGAGTCGACAGCCCTTAGAGATGTG 522
Qy 174 ValThrGlnTyrAlaIleValAspAsnPhePheGluLysAsnMetProLysPheLysGlu 193
Db 523 CGAAATCGATTTGAATCTCGATAGTTTATTATTCGCAATATATGCCATCTTTTAGAGTG 582
Qy 194 ArgAsnPheGluIleLeuLeuLeuProValTrpAlaGlnAlaAlaAsnLeuHisLeuIle 213
Db 583 ACAAAATTTTGAAGTACCATTCTCTGTATATGCAATGGGAGCCCAACCTTCATTTACTG 642
Qy 214 LeuLeuArgAspAlaAspTyrPheGlyAlaGlnTrpGlnLeuGlyAspGluIleArg 233
Db 643 TTATTAAGGACGGCTCAATTTTGGAGAGAAATGGGATGGTCAACACTACTATTATTAAT 702
Qy 234 AspAsnTyrIleArgLeuGlnGlyIleArgGluTyrLysAspHisCysIleThrPhe 253
Db 703 AACTATTATGATCGTCRAATGAACTTACTCCAGAAATATTCTCGATCACTGTGTAAGTGG 762
Qy 254 TyrAsnGlnGlyLeuAsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsn 273
Db 763 TATGAACTGGTTTATGCAAAATTTAAAGGACGACGCGCTAAACAACTGGTGTACTATAAC 822
Qy 274 ArgPheArgThrAspMetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyr 293
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Db	823	CAATTCCTGAGAGAAATGACACTGGCGGTTTTAGATGTTGTCGATTATTATCCCAAAATTAT	882
Qy	294	AspProArgArgTyrProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAsp	313
Db	883	GACACACGCGTACCCCAATGGAAACGAAAGCACAACTTAACAGGGAAGTATATACAGAT	942
Qy	314	ProValGlyPheThrGlyValLeuGluSerGlyGlyArgThrTyrProTfTyrAsnPro	333
Db	943	CCACTGGGCGCGTAACCGTGTCTTCAAATTTGGTTCC-----TGGTATGAC---	987
Qy	334	AsnAsnThrThrPheThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrThr	353
Db	988	AAAGCACCCTCTTTTCGGAGTGATAGAAATCATCGTTATTCCAGCACCCCAATGATTGTGAT	1047
Qy	354	TrpLeuAsnArgIlePheValTyrThr-----ArgThrLeuGlyAsnMetSerAspVal	371
Db	1048	TATATAACGGGACTCACAGTGTATACAAATCAAGAGCATTTCTTCGCTCGCTATATA	1107
Qy	372	ArgAsnIleTrpGlyGlyHisThrLeu-----ValGluAsnGlyAsnAspGlySerGluIle	390
Db	1108	AGACAT---TGGGCTGCTCATCAAAATAGCTACCATCGTCGTAGTAGGGGTAGTAATCTT	1164
Qy	391	ThrHisAsnPheGlyIysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsn	410
Db	1165	CAACAAATGATGGAACATAATCAAAATCTACACGCACTAGTACCTTTGATTTCAGCAAT	1224
Qy	411	LeuSerValPheSerIleGluSer-----LeuAlaArgIleTyrLeuGly	425
Db	1225	TATCATATTACAGACTCTATCAAGGATGCAGTACTCTCTGATATTGTTTACCTGGT	1284
Qy	426	GlyThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSerArgVal-----IlePhe	444
Db	1285	TATACG-----TATATATTT-----TTTGGAAATGCCAGAAATCGAGTTTTC	1326
Qy	445	AsnThrSerAsnIleAsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeu	464
Db	1327	ATGGTAACCAATTTGAATATACAGAAAGACGTTAAAGTAT-----AATCCA	1374
Qy	465	ProSerGlnThrIleLeuSer-----GluLeuProGlyLysAsp	477
Db	1375	GTITCCAAAGATATTATAGCGAGTACAGAGATTCGGAAATTAGAAATTACTCCAGAACT	1434
Qy	478	LysProArgProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAsp	497
Db	1435	TCAGATCAACCAATATTAGTATAGTACCATAGCATAGATTATGTCATATCAACGATTCC	1494
Qy	498	AlaArgArgSerSerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThr	517
Db	1495	GCACGGGTAACTACCGGATTAGTACCT-----GTATTTTCTTGACACATCGA	1545
Qy	518	SerMetAspArgAsnAsnArgLeuGluProAspIlyIleThrGlnIleAspAlaValLys	537
Db	1546	AGTGCAGATTAAACAATACATATATTCAGATAAAATCACTCAAAATTCGGCGCGTTAA	1605
Qy	538	GlyTrpGlyGlyAsnIleGlyPheValIle-----ProGlyProThrGlyGly	553
Db	1606	TGTTGG---CATAAATTTACCGTTTGTTCAGTGGTAAAGCAGCAGCATACAGAGGG	1662
Qy	554	AsnLeuValLysValSerAspSerTrpHisSerLeuLysVal-----	567
Db	1663	GAATTTATACAGTATATAGAAAGTACTGGTTCTGTAGAACCTTATTTCTAGCTCGATAT	1722
Qy	568	---GlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuVal	586
Db	1723	GGCCTAGCATTTAGAAAAAGCAGGAAATATCGTGTAAAGCTGAGATATGCTACT----	1776
Qy	587	ThrHisGlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPhePhe	606
Db	1777	-----GATGCAGATATTGTTATTCATGTAAACGATGCTCAGATTTCAG-----	1818
Qy	607	AspCysSerAsnSerSerGlyAlaArgProSerAsnThrLeuLeuGluSerAspPheArgTyr	626

Db 121 GATTATAAGAGTATTATTAATAATGCT-----GCGGHAATGCTAGT 162
Qy 63 ThrTyr-----SerSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 163 GAATACCTCGTGGTTCACCTCGAAGTACTTGTAGCGGACAGATGCGAGTAAAGCGCAAT 222
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
Db 223 GATATAGAGTAAATTAATCTACGTGTAGGGGTCCTCAATTTGTTGGCGCGATGAGT 282
Qy 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
Db 283 CTTTATACTCAACTTATTGATATTCTGTGGCCTTCAGGGGAAAGAGTCAATGGGAAATT 342
Qy 120 LeuMetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
Db 343 TTTATGGAACAAAGTAGAAGAACTATTATCAAAAATAATAGCAGAAATATGCAAGGAATAAA 402
Qy 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 403 GCGCTTTCGGAATTAGAGGATTAGGTAAATAATTACCAATTATATCTTAACTCGCGCTTGAA 462
Qy 160 AlaTrpLeuValAsnLysAsnAspAsnArg-----ArgAlaLeuVal 174
Db 463 GAATCGGAAGAAATCCAAATGGTTCAGAAATGGTTCGCGGCTTACGAGATGCGCA 522
Qy 175 ThrGlnTyrAlaIleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArg 194
Db 523 AATCGATTGGAATCCTGATAGTTATTTAGGCAATATATGCCATCTTTTAGAGTGACA 582
Qy 195 AsnPheGluIleLeuLeuLeuProValTyrAlaGlnAlaAsnLeuHisLeuIleLeu 214
Db 583 AATTGTGAAGTACCATTCTTACTGTATATGCAATGGCAGCCCACTTCATTTACTGTGA 642
Qy 215 LeuArgAspAlaAspTyrPheGlyAlaGlnTrpGlnLeuGlyAspGluIleArgAsp 234
Db 643 TTAAGGAGCGCTCAATTTTGGAGNAGNATGGGATGGTCAACAACACTATTATTAATAC 702
Qy 235 AsnTyrIleArgLeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyr 254
Db 703 TATTATGATCGTCAAAATGAACTTACTGCAAGATATCTGATCACTGTGTAAGTGGTAT 762
Qy 255 AsnGlnGlyLeuAsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArg 274
Db 763 GAACTGGTTAGCAAAATTAAGGACGACGCGCTAAACAATGGGTGACTATTAACCAA 822
Qy 275 PheArgThrAspMetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAsp 294
Db 823 TTCCGTAGNAAATGACACTGCGGCTTTAGATGTTGTTCATTTATTCCTCAATTTATGAC 882
Qy 295 ProArgArgTyrProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspPro 314
Db 883 ACACGCGTACCCCACTGAAACGAAAGCAACAACCTAAACAAGGAAGTATATACAGATCCA 942
Qy 315 ValGlyPheThrGlyValLeuGluSerGlyArgThrTyrProTyrTrpAsnProAsn 334
Db 943 CTGGCGCGGTAAACGCTGTTCAATGTGTTCC-----TGGTATGAC---AAA 987
Qy 335 AsnThrThrPheThrAlaMetGluAsnAlaArgArgArgProSerTyrThrTrp 354
Db 988 GCACCTTCTTCGGAGTATAGAAATCATCCGTTATTCGNACCACCCCATGATTTCATAT 1047
Qy 355 LeuAsnArgIlePheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArg 372
Db 1048 ATAACGGGACCTCACAGTGATACAAATCAAGAAGCATTTCTCCGCTCGCTATATAAGA 1107
Qy 373 AsnIleTrpGlyGlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThr 391
Db 1108 CAT---TGGCGTGGTCACTAAATAAGTACCACCTGTCAGTAGGGGTAGTAATCTTCAA 1164
Qy 392 HisAsnPheGlyLysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeu 411

Db 1165 CAATGTATGGAACCTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATTAT 1224
Qy 412 SerValPheSerIleGluSer-----LeuAlaArgIleTyrLeuGlyGly 426
Db 1225 GATATTTCAAGACTCTATCAAGAGATGCACTCTCTTGATATTGTTTACCTCGGTAT 1284
Qy 427 ThrGluAlaAsnAsnTyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsn 445
Db 1285 ACG-----TATATATTT-----TTTGGATGCCAGAGTCGAGTTTTCATG 1326
Qy 446 ThrSerAsnIleAsnAsnValProGlySerLeuArgTyrGluValProAlaAsnLeuPro 465
Db 1327 GTAAACCAATTGAATATACCAAGAAAGACGTTAAAGTAT-----AATCCAGTT 1374
Qy 466 SerGlnThrIleLeuSer-----GluLeuProGlyLysAspLys 478
Db 1375 TCCAAGATATATATAGCGAGTACAGAGATTCCGGAATTAGAAATACCTCCAGAAACTTCA 1434
Qy 479 ProArgProAsnAlaGlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAla 498
Db 1435 GATCAACCAATTTAGTCAATATAGCATATAGCATATATGTCATATCACAAGTATCCCGG 1494
Qy 499 ArgArgSerSerGlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSer 518
Db 1495 ACGGTAACTACCTCCGGATTAGTACCT-----GTATTTCTTGGACACATCGAAGT 1545
Qy 519 MetAspArgAsnAsnArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGly 538
Db 1546 GCAGATTTAAACAATACATAATATATTCAGATAAAATCACTCAAAATTCGCGCGCTTAAATGT 1605
Qy 539 TrpGlyGlyAsnIleGlyPheValIle-----ProGlyProThrGlyGlyAsn 554
Db 1606 TGG---GATAATTTACCGTTTGTCCAGTGTGTAAGGACCAAGACATACAGAGGGAT 1662
Qy 555 LeuValLysValSerAspSerTrpHisSerLeuLysVal-----567
Db 1663 TTATTACAGTATATAGAAAGTACTGGTCTCTAGGAACCTTATTATTCTAGCTCGATATGCG 1722
Qy 568 GlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThr 587
Db 1723 CTAGCATTTAGAAAAGCAGGGAATATCTGTAAAGACTGAGATATGCTACT-----1773
Qy 588 HisGlyAspAlaIlePheValGluHisSerGlySerHisIleValSerPhePheAsp 607
Db 1774 -----GATGAGATATTGATTTGATGTAACGATGCTCAGATTCAG-----1815
Qy 608 CysSerAsnSerSerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIle 627
Db 1816 --ATGCCAAAACAATGAACCCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTTGCA 1872
Qy 628 AspValProGlyIlePheThrProSerIleAsnProLeuIleArgTyrArg-----644
Db 1873 GATGCTATCACAACTTAAATTTAGCAACAGATAGTTCCGTAGCATTTGAAACATATTTA 1932
Qy 645 -----ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIle 659
Db 1933 GGTGAAGACCTAATTTCAACATTTCTGGTATAGTTTACGTTGACCGGAATCGAATTCATC 1992
Qy 660 ProLeuAsn 662
Db 1993 CCAGTAGAT 2001
RESULT 14
US-11-058-727-25
; Sequence 25, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen


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QY 539 TrpGlyGlyAsnIleGlyPheValIle-----ProGlyProThrGlyGlyAsn 554
Db 1606 TGG-----GATAATTTACCGTTTGTTCAGTGGTAAAGGACCAGGACATACAGGAGGGAT 1662

QY 555 LeuValLysValSerAspSerTrpHisSerLeuLysVal----- 567
Db 1663 TTATTACAGTATAAATAGAGTACTGGTTCTGTAGGAACCTTATTCTAGCTCGATATGGC 1722

QY 568 GlnAlaProGlnArgGlnThrSerTyrArgIleArgLeuArgTyrAlaCysLeuValThr 587
Db 1723 CTAGCATTTAGAAAACAGCGGAATATCTGTGAAGACTGAGATATGCTACT----- 1773

QY 588 HisGlyAspAlaIlePheValGluHisSerGlySerSerHisIleValSerPhePheAsp 607
Db 1774 -----GATGCAAGATTGTATGTCATGTAAACGATGCTCAGATTGAG----- 1815

QY 608 CysSerAsnSerSerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIle 627
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RESULT 15
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; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2022)
US-11-058-727-29

Alignment Scores:
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Score: 925.00 Matches: 239
Percent Similarity: 50.5% Conservative: 116
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Best Local Similarity: 34.0% Mismatches: 268
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US-10-782-096-2 (1-682) x US-11-058-727-29 (1-2022)

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QY 373 AsnIleTyrGlyGlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThr 391
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QY 392 HisAsnPheGlyThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeu 411
Db 1165 CAAATGTATGGAACCTAATCAAAATCTACAGCAGCTAGTACCTTTGATTTTACGAATTAT 1224
QY 412 SerValPheSerIleGluSer-----LeuAlaArgIleTyrLeuGlyGly 426
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Job time : 366 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 20, 2006, 22:28:18 ; Search time 9349 Seconds
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Listing first 45 summaries

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ALIGNMENTS

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DEFINITION CQ868318
ACCESSION CQ868318
VERSION CQ868318.1 GI:51998364
KEYWORDS Bacillus thuringiensis
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ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 19 02-SEP-2004;
Athenix Corporation (US)
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US-10-782-096-2 (1-682) x CQ868318 (1-2049)

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Db 2041 ATCAAT 2046

RESULT 2
CQ868320
LOCUS CQ868320 2016 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 21 from Patent WO2004074462.
ACCESSION CQ868320
VERSION CQ868320.1 GI:51998366
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE

1 Carozzi, N., Hargies, T., Kozel, M.G., Duck, N.B. and Carr, B.
Delta-endotoxin genes and methods for their use
Patent: WO 2004074462-A 21 02-SEP-2004;
Athenix Corporation (US)

FEATURES

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ORIGIN

Alignment Scores:
Pred. No.: 6,82e-255 Length: 2016
Score: 3536.00 Matches: 671
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 98.3% Indels: 0
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US-10-782-096-2 (1-682) x CQ868320 (1-2016)

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Db 1981 AGAGAACAGGAAGTAAATGATCTATTTATCAAT 2013

RESULT 3
CQ868322
LOCUS CQ868322 1986 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 23 from Patent WO2004074462.
ACCESSION CQ868322
VERSION CQ868322.1 GI:51998368
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.

TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 23 02-SEP-2004;
Athenix Corporation (US)
FEATURES
Location/Qualifiers
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Alignment Scores:
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Score: 3488.00 Matches: 661
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.0% Indels: 0
DB: Gaps: 0
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RESULT 5
LOCUS CS132867 3621 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 5 from Patent WO2005063996.
ACCESSION CS132867
VERSION CS132867.1 GI:71791818
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
1 Abad, A.
AUTHORS Plant activation of insect toxin
TITLE Patent: WO 2005063996-A 5 14-JUL-2005;
JOURNAL E.I. Du pont de nemours and company (US); Pioneer Hi-Bred International, Inc. (US)

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Query Match: 26.4% Indels: 78
DB: 6 Gaps: 25

US-10-782-096-2 (1-682) x CS132867 (1-3621)

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QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
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Qy 592 IlePheValGluHisSerGlySerSerHisIleValSerPhePheAspCysSerAsnSer 611
Db 1768 GATATGTTATGTCATGTAAACGATGCTCAGATTTCAG-----ATGCCAAA 1812
Qy 612 SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIleAspValProGly 631
Db 1813 ACAATGAACCCGAGGTGAGGATCTGACATCTAAACATTTTAAAGTTGCAGATGCTATCACA 1872
Qy 632 IlePheThrProSerIleAsnProLeuIleArgTyrArg----- 644
Db 1873 ACATTAATTTAGCAACAGATAGTTCGTAGCATTTGAAACATAATTTAGTGAAGACCT 1932
Qy 645 ---ThrGlnSerPheGlyThrHisAlaIleAspLysPheGluPheIleProLeuAsn--- 662
Db 1933 AATTCACATATCTGTTATAGTTTACCTGACCGAATCGAATTCATCCAGTAGATGAG 1992
Qy 663 ThrPhe---ProAsnGlnSerLeuGluLysArgGluGlnGluValAsnAspLeuPheIle 681
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LOCUS CS130962 4874 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 17 from Patent WO2005066349.
ACCESSION CS130962
VERSION CS130962.1 GI:71793198
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
REFERENCE 1
AUTHORS Abad,A.
TITLE Genes encoding proteins with pesticidal activity
JOURNAL Patent: WO 2005066349-A 17 21-JUL-2005;
E.I. Du pont de nemours and company (US); Pioneer Hi-Bred
International, Inc. (US)
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Query Match:	26.4%	Indels:	78	
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QY	23	SerAsnGlyTyrProArgTyrProLeuAlaLysAspProGlnMetMetArgAsnThr	42	
DB	791	TCCAAATGATCTTAACAGATACCTTTTGCAGATGAGCCAAACAAATGCGCTACAAAATATG	850	
QY	43	AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspLeuSer	62	
DB	851	GATTAATAAGATATTTAAATGCTCT-----GCGGGAATGCTAGT	892	
QY	63	ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle	81	
DB	893	GAAATACCTCGTTTCACTGAGTACTTGTAGCGGCAAGATGCGAGTAAAGCCGCAATT	952	
QY	82	AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly	101	
DB	953	GATATAGTAGGTAATATCTATCTAGCTTTTGGGGTCCCATTTTGTGGCCGATAGT	1012	
QY	102	IleIleSerArgLeuIleGlyLeuTrpAlaGlyProAsp-----ProPheGluAla	119	
DB	1013	CTTTATCTCACTTATTGATATCTGTGGCCCTCAGGGGAAAGAGTCAATGGGAATT	1072	
QY	120	LeuMetValLeuGluGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn	139	
DB	1073	TTTATGGAACAGTAGAAGACTCATTAATCAAAAATATGACAGATATGCAAGGAATAAA	1132	
QY	140	AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln	159	
DB	1133	CGCTTTTCGGAATTAGAAGGATAGGTAAATTAATTAACCAATTATCTAACTCGCGTTGAA	1192	
QY	160	AlaTrpLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla	178	
DB	1193	GAATGGGAAGAAATCCAAATGGTTCAAGAGCTTACGAGATGTGCGAAATCGATTGAA	1252	
QY	179	IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle	198	
DB	1253	ATCTCGATAGTTTATTTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTA	1312	
QY	199	LeuLeuLeuProValTyrAlaGlnAlaAlaLeuHisLeuIleLeuLeuArgAspAla	218	
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QY	219	AspTyrPheGlyAlaGluTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg	238	
DB	1373	TCAATTTTGGAGAAGAAATGGGATGGTCAACAACTACTATTAACTATTATGATCGT	1432	
QY	239	LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu	258	
DB	1433	CAAAATGAACTTACTGCGAGATATCTGATCACTGTGTAAAGTGTGTGAACCTGGTTTA	1492	
QY	259	AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp	278	
DB	1493	GCAAAATTTAAAGGACGAGCGCTAAACAAATGGGTGACTATAACCAATTCGCTAGAGA	1552	
QY	279	MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgTyr	298	
DB	1553	ATGACACTGGCGGTTTATAGATGTTTTCGATTTATTTCCCAATTTATGACACGACGCTAC	1612	
QY	299	ProLeuAlaValLeuThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr	318	

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QY	359	PheValTyrThr-----ArgThrLeuGlyAsnMetSerAspValArgAsnIleTrpGly	376	
DB	1778	ACAGTGATATACAAATCAAGAACATTTCTTCGCTCGCTATATAAGACAT---TGGGCT	1834	
QY	377	GlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGly	395	
DB	1835	GGTCATCAATTAAGCTACCATCGTGTCTAGTAGGGTAGTAATCTTCAACAAATGTATGGA	1894	
QY	396	LysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSer	415	
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QY	416	IleGluSer-----LeuAlaArgIleTyrLeuGlyGlyThrGluAlaAsn	430	
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AX543950
LOCUS AX543950 4874 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 27 from Patent WO0234774.
ACCESSION AX543950
VERSION AX543950.1 GI:25277423
KEYWORDS
SOURCE
ORGANISM Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1
REFERENCE
AUTHORS Abad,A.R., Duck,N.B., Feng,X., Flannagan,R.D., Kahn,T.W. and
Sims,L.E.
TITLE Genes encoding novel proteins with pesticidal activity against
coleopterans
JOURNAL Patent: WO 0234774-A 27 02-MAY-2002;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
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ORIGIN

Alignment Scores:
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Score: 948.00 Matches: 248
Percent Similarity: 50.9% Conservative: 119
Best Local Similarity: 34.4% Mismatches: 276
Query Match: 26.4% Indels: 78
DB: 6 Gaps: 25

US-10-782-096-2 (1-682) x AX543950 (1-4874)
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Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
Db 791 TCCAAATGATTCTAACAGATACCTTTTCGGAATGAGCAACAAATGCGCTACAAAATATG 850
Qy 43 AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer 62
Db 851 GATTATAAAGATATTATTAATAATGCT-----GCGGGAATGCTAGT 892
Qy 63 ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
Db 893 GAATACCTCGTTTCACTGAGTACTTGTAGCGGCAAGATGAGCTAAGGCCCGCAATT 952
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101.
Db 953 GATATAGTAGGTAAATATCTACGTTTAGGGTCCCAATTTGTTGGGCGCATAGTAGT 1012
Qy 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyProAsp-----ProPheGluAla 119
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Bacillus thuringiensis kumamotoensis PS50C(b) CryIII			
delta-endotoxin gene, partial cds.			
ACCESSION			
U04365			
VERSION			
U04365.1 GI:436834			
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SOURCE			
ORGANISM			
Bacillus thuringiensis			
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus			
cereus group.			
1 (bases 1 to 3507)			
Narva, K.E. and Fu, J.			
Novel Coleopteran-Active Toxins from Bacillus thuringiensis			
JOURNAL			
Unpublished (1994)			
REFERENCE			
2 (bases 1 to 3507)			
Feitelson, J.S.			
AUTHORS			
Direct Submission			
TITLE			
Submitted (15-DEC-1993) Gerald S. Feitelson, Molecular Biology,			
JOURNAL			
Mycogen Corporation, 4980 Carroll Canyon Road, San Diego, CA 92121,			
USA			

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		WNTTSYVNVQIINHSTSLVLIIPNNEQVSQKFTVQPNQRYVLRVTRKEGVNGYVIR	
		DGNQSEITLFSADYIDNGYDTQASNTINGINTNSYIMLKPAISRKITVDISSVTNQM	
		WIEISETEGTFYIESVELVDVE"	
ORIGIN			
Alignment Scores:			
Pred. No.:		1.45e-60	
Score:		942.50	
Percent Similarity:		50.3%	
Best Local Similarity:		34.4%	
Query Match:		26.2%	
DB:		1	
Gaps:		27	
US-10-782-096-2 (1-682) x BTU04365 (1-3507)			
Qy	3	SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet	22
Db	4	AGTCCAAATAATCAAAATGAATATGAAATATATAGATGCGACACCT---TCTACATCTGTA	60
Qy	23	SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr	42
Db	61	TCCAATGATTCTAACAGATACCCCTTTTCGGAATGAGCCACAAATGCGCTACAAAATATG	120
Qy	43	AsnTyrLysGluTrpLeuAsnMetCysAspSerAsnThrGlnPheIleGlyAspIleSer	62
Db	121	GATTATAAGATTATTTAAAAATGTCT-----GCGGGAATGTTAGT	162
Qy	63	ThrTyr---SerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle	81
Db	163	GAATACCTGGTTCACCTGAGGTATTTCTAAGCAGCAAGATGCGATTAGGCCGCAATT	222
Qy	82	AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaIleSerGlnSerPheGly	101
Db	223	GATATAGTAGGTAAATTAATTAACAGGTTTAGGGGTTCATTTGTTGGCCCGATAGTAGT	282
Qy	102	IleIleSerArgLeuIleGlyIleLeuTrpAlaGly-----ProAspProPheGluAla	119
Db	283	CTTTATACTCAACTATTGATATTTCTGTGGCCTTCAAAACAAAGAGATCAATGGAAATT	342
Qy	120	LeuMetValLeuValGluGluLeuIleLysLysSerIleAspGlnArgValArgLeuAsn	139

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Db 343 TTTATGGAACAAGTAGAAGAACTCTTAATCAAAAATAGCAGATATGCAAGGATATAA 402
Qy 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
Db 403 GCGCTTTTCGGAATTCGGAAGGCTAGGGAATAATATACCAATATATATCTAACTGCGCTGAA 462
Qy 160 AlaTrpLeuValAsnLysAsnAspAsnArg---ArgAlaLeuValThrGlnTyrAla 178
Db 463 GAGTGGAAAGAAATCCAAATGGTTTCAAGAGCCTTACAGAGATGTTTCGAAATCGAATTGAA 522
Qy 179 IleValAspAsnPheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
Db 523 ATCTCGGATAGTTATTTACGAATATATGCAATATGCACTCTTTTCGAGTCACAAATTTTCAGTA 582
Qy 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
Db 583 CCATTCTTTACAGTATATACAAATGCGCAGCAAACTTACATTTTACTTTTATTAAGGCGCA 642
Qy 219 AspTyrPheGlyAlaGlnTrpGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
Db 643 TCAATTTTGGAGAGAAATGGGATGTCTCAAGCACTATTATAAATACTACTATAATCGT 702
Qy 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
Db 703 CAATGAAACTTACTGCGAATAATTTCTGACCACCTGTGTAAGTGTATGAACTGGITTA 762
Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp 278
Db 763 GCAAAATTAAGGCTCGAGCGCTAAACAATGGATTGACTATACCAATTCGTTAGAGAA 822
Qy 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
Db 823 ATGACATTCGCGGTGTAGACGTTGTCATTTATTTTCAAACTATGATACGCGTACGTAT 882
Qy 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
Db 883 CCACCTGGCAACAACAGCTCAGCTTACAAGGGAAGTATATACAGATCCACCTTGGCGCGTA 942
Qy 319 GlyValLeuGluSerGlyLysArgThrTyrProTyrTyrAsnProAsnAsnThrThrPhe 338
Db 943 GATGTCCTTAATTTGGCTCC-----TGTATGAC---AAGCACCTTCCTTC 987
Qy 339 ThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrThrTrpLeuAsnArgIle 358
Db 988 TCAGAAATAGAAAAGCGCTATTGCTCCACTCATGTGTTTGTATATTAACGCGACTC 1047
Qy 359 PheValTyrThrArgThrLeuGlyAsnMetSerAsp---ValArgAsnIleTrpGlyGly 377
Db 1048 ACAGTTTATACAAAAAAGCTAGCTTCTCTGATCGTTATATGAGATATTTGGCGTGT 1107
Qy 378 HisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPheGlyLys 396
Db 1108 CATCAAAATAGCTATAGCATATCGTAGAGTAGTACTTTTACACAGATGTATGGAACC 1167
Qy 397 ThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPheSerIle 416
Db 1168 AATCAAAATTTACAAAGTACTAGCAATTTTGATTTTACCAATTTACGATATTTACAGACT 1227
Qy 417 GluSer-----LeuAlaArgIleTyrLeuGlyThrGluAlaAsnAsn 431
Db 1228 TTATCAAAATGGTCAGTACTCTCTGATATAGTTTACCTCGT----- 1269
Qy 432 TyrIleThrSerGlnTyrGlyValSerArgVal---IlePheAsnThrSerAsnIleAsn 450
Db 1270 TATAGTATACATTTTTTGGATGCGCAGAAACCGAGTGTATTTATGCTAAATCAATGAT 1329
Qy 451 AsnValProGlySerLeuArgTyrGluValProAlaAsnLeuProSerGlnThrIleLeu 470
Db 1330 AATACCAGAAAGACGCTTAACGTATATAA---CCAGCT-----TCCAAAGATATTATA 1377
Qy 471 Ser-----GluLeuProGlyLysAspLysPheProArgProAsnAla 483
Db 1378 GATCGGACACAGAGATTGCGAATTAGATTGCTTCCAGAAACTTTCAGGTCAACCAATTTAC 1437
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Qy 484 GlyAspPheSerHisArgLeuSerTyrIleSerAsnPheAspAlaArgArgSerSerSer 503
Db 1438 GAGTCATATACCATAGATAGATTAGTCAATATACATTTATT-----TACTCCAGT 1485
Qy 504 GlyGlyIleValSerLeuLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsnAsn 523
Db 1486 TCAACTAGCAGTATGTACCTGTATTTCTTTGGACACATCGGAGTGCAGATCTAACAAAT 1545
Qy 524 ArgLeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrpGlyAsnIle 543
Db 1546 ACAGTTAAAGCTGGGAAATCACCMAATACCAGG-----GGCAAGCTTAGCACCATTA 1599
Qy 544 Gly-----PheValIleProGlyPro-----ThrGlyGlyAsnLeuValLysVal 558
Db 1600 GCGCAAAATCTTATATAATAAAAGGCGTGTGTATATACAGGGGAGACTTAGTGGCTTTA 1659
Qy 559 SerAspSerTrpHisSerLeuLysValGlnAla-----ProGlnArgGlnThrSerTyr 576
Db 1660 ACGGACCGCATCGGAAGTTGTGAGTTTCAGATGATCTTTCCAGAGTCTCA---CGATTTC 1716
Qy 577 ArgIleArgLeuArgTyrAlaCysLeuValThrHisGlyAspAlaIlePheValGluHis 596
Db 1717 CGTATTCGATTCGTAGCT----- 1737
Qy 597 SerGlySerSerHisIleValSerPhePheAspCysSerAsnSer----- 611
Db 1738 TCTAATGAAACTAGTTATATATTAGTTTATACGAGCTAAACCAAGCGGAACCTTTAAATTC 1797
Qy 612 -----SerGlyArgProSerAsnThrLeuLeuGluSerAspPheArgTyrIle 627
Db 1798 AACCAGACATATTTCTAATAAAAAATGAAATGATTTAACAATATATGATTTCAATATATA 1857
Qy 628 AspValProGlyIlePheThrProSerIleAsnProLeuIleArgTyrArgThrGlnSer 647
Db 1858 GAATATCCAGAGTCATT-----TCAGTAATGCTTCTTCAACATACAGAGTTACT 1911
Qy 648 PheGlyThrHisAla-----IleAspLysPheGluPheIleProLeu 661
Db 1912 ATAGGTATACAAACGAATACAAATTTATTTATTTTAGACCAATTCGAATTCATCCAGTA 1971
Qy 662 Asn---ThrPheProAsnGlnSer---LeuGluLysArgGluGlnValAsnAspLeu 679
Db 1972 GATGACATATGAGCGGAACCGATTTAGAGCGCAAGAGTGAAGCGCAAGAGTGAATGCTT 2031
Qy 680 PheIleAsn 682
Db 2032 TTTAGCAAT 2040

RESULT 10
LOCUS I25972 3507 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 3 from patent US 5554534.
ACCESSION I25972
VERSION I25972.1 GI:1605842
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3507)
AUTHORS Michaelis,T.E., Narva,K.E. and Foncerrada,L.
TITLE Bacillus thuringiensis toxins active against scarab pests
JOURNAL Patent: US 5554534-A 3 10-SEP-1996;
FEATURES
source
1..3507
/organism="unknown"
/mol_type="unassigned DNA"

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Pred. No.: 942.50 Matches: 249
Score: 50.3% Conservative: 115
Percent Similarity:
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Db 1972 GATGACATATGAAGCGGAACGATTTAGAAAGCGGCAAGAAAGCAGTGAATGCCTTG 2031
Qy 680 PheIleAsn 682
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Db 2032 TTTACGAAT 2040

RESULT 11
LOCUS BD133574
DEFINITION protein having insecticidal activity, DNA encoding the protein, and
controlling agent and controlling method of noxious organisms.
ACCESSION BD133574
VERSION BD133574.1 GI:23228519
KEYWORDS JP 2002045186-A/1.
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
1 (bases 1 to 3504)
AUTHORS Asano,S., Yamanaka,S. and Takeuchi,K.
TITLE protein having insecticidal activity, DNA encoding the protein, and
controlling agent and controlling method of noxious organisms
JOURNAL Patent: JP 2002045186-A 1 12-FEB-2002;
SDS BIOTECH KK
COMMENT
OS Bacillus thuringiensis
PN JP 2002045186-A/1
PD 12-FEB-2002
PF 03-AUG-2000 JP 2000236140
PI SHINICHIRO, ASANO, SATOSHI YAMANAKA, KATSUYOSHI TAKEUCHI PC
C12N15/09, A01N63/00, A01N63/02, C07K14/325, C12N1/15, C12N1/19, PC
C12N1/20,
PC C12N1/20, C12N1/21, C12N5/10, C12N5/10/(C12N15/09, C12R1/19), PC
(C12N1/20, C12R1/07), C12N15/00, C12N5/00, C12N5/00, (C12N15/00, PC
C12R1/19)
CC protein having insecticidal activity, DNA
encoding the protein,
and
CC controlling agent and controlling method of noxious organisms
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
1..3504
/organism="Bacillus thuringiensis"
/mol_type="genomic DNA"
/db_xref="taxon:1428"

FEATURES
source
Location/Qualifiers
1..3504
2,05e-60 Length: 3504
940..50 Match: 256
51.8% Conservative: 111
36.1% Mismatches: 288
26.1% Indels: 56
6 Gaps: 23

ORIGIN
US-10-782-096-2 (1-682) x BD133574 (1-3504)

Alignment Scores:
Pred. No.: 2.05e-60 Length: 3504
Score: 940..50 Match: 256
Percent Similarity: 51.8% Conservative: 111
Best Local Similarity: 36.1% Mismatches: 288
Query Match: 26.1% Indels: 56
DB: 6 Gaps: 23

US-10-782-096-2 (1-682) x BD133574 (1-3504)

Qy 3 SerTyrLysAsnLysAsnGluTyrGluMetLeuAspAlaLeuArgIleAsnSerAsnMet 22
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Db 4 AGTCAAAATATCAAAATGAATATGAATATGAATATGAATATGAATATGAATATGAAT 60
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 61 TCCGGAATATCTGTATGATACCTTTAGCAACGATCAACGACCAATACAAACATG 120
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 43 AsnTyrLysGluTyrLeuAsnMetCysAsp---SerAsnThrGlnPheIleGlyAspIle 61
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 121 AACTATAAGATATCTGAGATGCTCGAGGAGAGATCTGATATTTTGGAAATCGG 180
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 62 SerThrTyrSerProGluAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||

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Db 181 GAGACGTTTATTAGT-----TCATCTACGGTTCAAACTGGAATT 219
Qy 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 220 GGCATTGTGTCAAGTACTGGGGCTTTAGGGGTTCCATTTCCTGGACAGATAGTAGT 279
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 102 IleIleSerArgLeuIleGlyIleLeuTyrPalaGlyPro-----AspProPheGluAla 119
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 280 TTTTATAGTTTCATTGTGCGTCAATTATGGCCATCAAGTACCGTGAGTGATGGGAAATG 339
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 120 LeuMetValLeuValGluGluLeuIleLysSerIleAspGlnArgValArgGluAsn 139
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 340 ATTATGAACAAGTGAAGATCTAATTCATCAAAAATAACAGATCTCTGTAAAGGAAACA 399
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Qy 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 400 GCGCTTGCGGACTACAAAGGATTAGGAGATGGCTTAGACGTATATCAGAAATCACTTAAG 459
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Qy 160 AlaTyrLeuValAsnLysAsnAspAsnArgArgAla---LeuValThrGlnTyrAla 178
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 460 AATTGGCTGGAAAATCGTAATGATCAAGACTAGAAAGTGTGTGGTGACCCAAATATATA 519
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 179 IleValAspAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 520 GCTTTAGAGCTGATTTTGTGCTAAATCCATCTTTTGCATATATCGGACAGAGATA 579
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 580 CCATTATTATCAGTGTATGCACAAGCAGCGAATTTACATTTTCTATTATTACGAGATGCT 639
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 219 AspTyrPheGlyValGlnTyrGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 640 TCCATTTTGGAGCAGAGTGGGGATTCACACGAGGAGAAATTTCCACATTTTATGATCGT 699
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysValIleThrPheTyrAsnGlnGlyLeu 258
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 700 CAGGTGACACGTACCGCCCAATACCTCGGATTTATGTGTAAGTGGTATAACACTGGCTTA 759
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTyrValSerPheAsnArgPheArgThrAsp 278
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 760 GATAAATTAAAGGTACGAATGCTGCAAGTTGGCTGAAGTATCACCAATTCGGAAGAGAA 819
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 279 MetThrLeuThrValLeuAspLeuAlaIleLeuPheProAsnTyrAspProArgArgTyr 298
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 820 ATGACATTACTGTTAGATTTAGTACGCTTATTTCCAAAATATGACACACGATCGTAT 879
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 299 ProLeuAlaValLysThrGluLeuThrArgGluValTyrThrAspProValGlyPheThr 318
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 880 CCAATCGAACAACGCGCCCACTTACCGGGAAGTGATACAGATCCCAATAGTATTTAAC 939
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 319 GlyValLeuGluSerGlyArgThrTyrProTyrAsnProAsnAsnThrThrPhe 338
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
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Qy 339 ThrAlaMetGluAsnAsnAlaArgArgArgProSerTyrThrThrTyrLeuAsnArgIle 358
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
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Qy 359 PheValTyrThrArgThrLeuGly-----AsnMetSerAspValArgAsnIleTyr 375
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
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Qy 376 GlyGlyHisThrLeu---ValGluAsnGlyAsnAspGlySerGluIleThrHisAsnPhe 394
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 1117 GTAGACATCTATAAATAATAAATAACGAATGCCTCATCAGCATTAGAACGTAATTAC 1176
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 395 GlyLysThrAspSerIleThrProIleGlnTyrPheAsnPheAlaAsnLeuSerValPhe 414
   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
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   ||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Qy 415 SerIleGluSerLeuAlaArgIleTyrLeuGlyThrGluAlaAsnAsnTyrIleThr 434
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QY 435 SerGlnTyrGlyValSerArgValIlePheAsnThrSerAsnIleAsnValProGly 454
DB 1276 CAGGTATATGGAGTTCGCTACCTAGTATTTTACCTGCTTGACAAGATACAGATCAGA 1335
QY 455 SerLeu-----ArgTyrGluValProAlaAsn-----LeuProSer 466
DB 1336 TCAGTTGGAGGTTTACGTTACTCAAAACCACATACATCAAGTATGTACACAAAT 1395
QY 467 GlnThrIleLeuSerGluLeuProGlyLysAspLysProArgProAsnAlaGlyAspPhe 486
DB 1396 TACAATACGATTGATGAATCCCTCCAGAGAATGAGCCACTTAGTAGAGG-----TAT 1449
QY 487 SerHisArgLeuSerTyrIleSer-----AsnPheAspAlaArgSerSerGly 504
DB 1450 AGCCATAGATTAATCATATACCTCTTATTTCTTAAAGATGCTAGTAGTCTGCT 1509
QY 505 GlyIleValSerLeuThrPheGlyTrpAlaHisThrSerMetAspArgAsnAsnArg 524
DB 1510 AGATATGGCAATCTCCCTGTAATTTGCTTGACACATCGAGTGGCATTTACAAATACA 1569
QY 525 LeuGluProAspLysIleThrGlnIleAspAlaValLysGlyTrp-----GlyGly 541
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QY 542 AsnIleGlyPheValIleProGlyProThrGlyGlyAsnLeuValIleValSerAspSer 561
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QY 562 -----TrpHisSerLeuLysValGlnAlaProGlnArgGlnThrSerTyrArg 577
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QY 618 ThrLeuLeuGluSerAspPheArgTyrIleAspValProGlyIlePheThr---ProSer 636
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QY 637 IleAsnProLeuIleArgTyrArgThrGlnSerPhe-----GlyThrHisAlaIle 653
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QY 672 ArgGluGlnGluValAsnAspLeuPhe 680
DB 2032 GCAGAAGAGCAGTAATAGCTTGT 2058
RESULT 12
BD133575 3690 bp DNA linear PAT 18-98P-2002
LOCUS Protein having insecticidal activity, DNA encoding the protein, and
DEFINITION controlling agent and controlling method of noxious organisms.
ACCESSION BD133575
VERSION BD133575.1 GI:23228520
KEYWORDS JP 2002045186-A/2.
SOURCE Bacillus thuringiensis
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE 1 (bases 1 to 3690)
AUTHORS Asano,S., Yamanaka,S. and Takeuchi,K.
TITLE Protein having insecticidal activity, DNA encoding the protein, and
controlling agent and controlling method of noxious organisms

JOURNAL Patent: JP 2002045186-A 2 12-FEB-2002;
SDS BIOTECH KK
COMMENT OS Bacillus thuringiensis
PN JP 2002045186-A/2
PD 12-FEB-2000
PF 03-AUG-2000 JP 2000236140
PI SHINICHIRO ASANO,SATOSHI YAMANAKA,KATSUYOSHI TAKEUCHI PC
C12N15/09,A01N63/00,A01N63/02,C07K14/325,C12N1/15,C12N1/19,PC
C12N1/20,
PC C12N1/20,C12N1/21,C12N5/10,C12N5/09,C12R1:19),PC
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CC Protein having insecticidal activity, DNA
encoding the protein,
and
CC controlling agent and controlling method of noxious organisms
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DB 247 TCCGATAATTCCTGTAGATACCTTTAGCAACAGATCAACAGCACATTAACAAACATG 306
QY 43 AsnTyrLysGluTrpLeuAsnMetCysAsp---SerAsnThrGlnPheIleGlyAspIle 61
DB 307 AACTATAAGATATTCGAGAATGCTCGAGGAGAGAATCTCTGAATATTATTTGGAATCCG 366
QY 62 SerThrTyrSerSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
DB 367 GAGACGTTTATAGT-----TCATCTACGTTTCAAACTGGAAT 405
QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
DB 406 GGCATGTTGCTCAAGTACTCGGGGCTTTAGGGGTTCCATTTGCTGGACAGATAGTAGT 465
QY 102 IleIleSerArgLeuIleGlyIleLeuTrpAlaGlyPro-----AspProPheGluAla 119
DB 466 TTTTATATTTTCAATTCGCTCAATATGCGCATCAAGTACCGTAGTGTATGGGAATG 525
QY 120 LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
DB 526 ATTATGAACCAAGTGGAAAGATCTAATTGATCAAAAATAACAGATCTTGTAAAGGAACA 585
QY 140 AlaLeuArgGluLeuGluGlyLeuGlnGlyIleMetArgLeuTyrGlnThrArgLeuGln 159
DB 586 GCGCTTCAGGACTACAAGGATAGGAGATAGGAGATGCTTAGACGTATATCAAAATCACTTAAG 645
QY 160 AlaTrpLeuValAsnLysAsnAspAsnArgAla---LeuValThrGlnTyrAla 178
DB 646 AATTGGCTGGAAATTCGTAATGATACAGAGCTAGAGCTTTGTGGTACCCCAATATA 705
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ORIGIN

Alignment Scores:
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Score: 930.50 Matches: 254
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Best Local Similarity: 35.9% Mismatches: 288
Query Match: 1 Indels: 56
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US-10-782-096-2 (1-682) x AB089299 (1-3435)

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QY 23 SerAsnCysTyrProArgTyrProLeuAlaLysAspProGlnMetThrMetArgAsnThr 42
DB 61 TCCGATAAATCTGTTAGATACCTTTAGCAACGATCAAAACACACACATTAACAAACATG 120

QY 43 AsnTyrLysGluTyrLeuAsnMetCysAsp---SerAsnThrGlnPheIleGlyAspIle 61
DB 121 AACTATAAGATTATCTGAGATGCTCGGGGAGAGATCTCGAATATTTGGAAATCGG 180

QY 62 SerThrTyrSerProGluAlaAlaLeuSerValArgAspAlaValLeuThrGlyIle 81
DB 181 GAGACGTTTATTAGT-----TCATCTACCGTTCAAACTGGAATT 219

QY 82 AsnSerValGlyThrIleLeuSerAsnLeuGlyValProLeuAlaSerGlnSerPheGly 101
DB 220 GGCATTGTGTGCAAGTACTGGGGCTTTAGGGGTTCCATTGTCTGGACAGATAGCTAGT 279

QY 102 IleIleSerArgLeuIleGlyLeuTyrAlaGlyPro-----AspProPheGluAla 119
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QY 120 LeuMetValLeuValGluLeuIleLysLysSerIleAspGlnArgValArgGluAsn 139
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QY 160 AlaTrpLeuValAsnLysAsnAspAspArgAla---LeuValThrGlnTyrAla 178
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QY 179 IleValAsnPhePheGluLysAsnMetProLysPheLysGluArgAsnPheGluIle 198
DB 520 GCTTTAGAGCTGATTGTTGCTAAAAATCCCATCTCTTTTGCATATATCTGCGACAGGAAGTA 579

QY 199 LeuLeuLeuProValTyrAlaGlnAlaAlaAsnLeuHisLeuIleLeuLeuArgAspAla 218
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QY 219 AspTyrPheGlyAlaGlnTyrGlnLeuGlyAspAspGluIleArgAspAsnTyrIleArg 238
DB 640 TCCATTTTGGAGCAGAGTGGGGATTCCACCAGGAGAAATTTCCACATTTTATGATCGT 699

QY 239 LeuGlnGlyLeuIleArgGluTyrLysAspHisCysIleThrPheTyrAsnGlnGlyLeu 258
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QY 259 AsnGlnPheAsnArgSerAsnAlaGlnAspTrpValSerPheAsnArgPheArgThrAsp 278
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DEFINITION Sequence 5 from Patent WO0234774.
ACCESSION AX543928
VERSION AX543928.1 GI:25277387
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1
REFERENCE
AUTHORS Abad,A.R., Duck,N.B., Peng,X., Flannagan,R.D., Kahn,T.W. and
Sims,L.E.
TITLE Genes encoding novel proteins with pesticidal activity against
coleopterans
JOURNAL Patent: WO 0234774-A 5 02-MAY-2002;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
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Pred. No.: 1,24e-59 Length: 2003
Score: 926.00 Matches: 239
Percent Similarity: 50.8% Conservative: 116
Best Local Similarity: 34.2% Mismatches: 268
Query Match: 25.7% Indels: 76
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US-10-782-096-2 (1-682) x AX543928 (1-2003)
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Search completed: January 21, 2006, 01:57:09
Job time : 9422 secs

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